



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 173123**

**TO: Ruixiang Li**  
**Location: REM/4D75/4C70**  
**Art Unit: 1646**  
**Thursday, December 15, 2005**  
**Case Serial Number: 10/061727**

**From: Kristine Hensle**  
**Location: Biotech-Chem Library**  
**REM-1B69**  
**Phone: (571) 272-4161**

**Kristine. Hensle@uspto.gov**

### **Search Notes**

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle  
Librarian  
STIC Biotech/Chem Library  
(571)272-4161

**This Page Blank (uspto)**

From: Li, Ruixiang  
Sent: Thursday, December 01, 2005 4:04 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/061,727

Please do a standard search on:

- (i).SEQ ID NO: 2 against interference amino acid databases;  
(ii). SEQ ID NOS: 1 and 2 against interference nucleic acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

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DEC - 1 2005  
STIC/BIOTECH LIBRARY  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 07:35:54 ; Search time 377 Seconds  
(without alignments)  
9731.796 Million cell updates/sec

Title: US-10-061-727-1  
Perfect score: 2064  
Sequence: 1 atgacactctctggtgtgtg.....acgacttttatatccctataa 2064

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88878028 residues  
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PPUS COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfilee1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1388.4	67.3	1740	3	US-08-991-944-1
2	1388.4	67.3	4724	3	US-09-949-016-313
3	1388.4	67.3	4726	3	US-09-949-016-5448
4	1073	52.0	2703	3	US-10-282-162-39
5	1073	52.0	2709	3	US-10-282-162-41
6	1073	52.0	2709	3	US-10-282-162-43
7	1069.6	51.8	2748	3	US-10-282-162-51
8	1069.6	51.8	2754	3	US-10-282-162-53
9	1069.6	51.8	2754	3	US-10-282-162-55
10	1069.2	51.8	2733	3	US-09-313-942-27
11	1069.2	51.8	2733	3	US-10-282-162-27
12	1067.4	51.7	3355	3	US-08-991-944-3
13	1017	49.3	2703	3	US-10-282-162-33
14	1017	49.3	2709	3	US-10-282-162-35
15	1017	49.3	2709	3	US-10-282-162-37
16	1015	49.2	2748	3	US-10-282-162-45
17	1015	49.2	2754	3	US-10-282-162-47
18	1015	49.2	2754	3	US-10-282-162-49
19	292.8	14.2	141454	3	US-09-949-016-12055
20	292.8	14.2	141455	3	US-09-949-016-17190
21	235.8	11.4	601	3	US-09-949-016-24207
22	235.8	11.4	601	3	US-09-949-016-190484
23	153.8	7.5	601	3	US-09-949-016-24225
24	153.8	7.5	601	3	US-09-949-016-190530

25	151	7.3	2061	3	US-09-173-151A-3	Sequence 3, Appli
26	149.8	7.3	601	3	US-09-949-016-24226	Sequence 24226, A
27	149.8	7.3	601	3	US-08-949-016-190531	Sequence 190531, A
28	149.4	7.2	601	3	US-09-949-016-24224	Sequence 24224, A
29	149.4	7.2	601	3	US-09-949-016-190515	Sequence 190515, A
30	144.4	7.0	2537	3	US-09-173-151A-34	Sequence 34, Appli
31	139.4	6.8	1737	3	US-09-173-151A-1	Sequence 1, Appli
32	96	4.7	229	3	US-09-513-999C-13178	Sequence 13178, A
33	89.6	4.3	1626	2	US-08-604-333-1	Sequence 1, Appli
34	89.6	4.3	1626	3	US-09-110-618-1	Sequence 1, Appli
35	89.6	4.3	1626	3	US-09-578-178-1	Sequence 1, Appli
36	89.6	4.3	1626	3	US-09-577-806-1	Sequence 1, Appli
37	89.6	4.3	1626	3	US-09-621-502-3	Sequence 3, Appli
38	88.6	4.3	1991	3	US-09-173-151A-19	Sequence 19, Appli
39	88.6	4.3	2220	3	US-09-949-016-2443	Sequence 2443, Ap
40	88	4.3	3522	3	US-09-023-655-906	Sequence 906, App
41	88	4.3	3522	3	US-09-949-002-74	Sequence 74, Appl
42	88	4.3	3522	3	US-09-949-002-203	Sequence 203, App
43	75.2	3.6	1563	3	US-08-996-338-1	Sequence 1, Appli
44	75.2	3.6	1563	3	US-09-556-972-1	Sequence 1, Appli
45	75.2	3.6	1620	3	US-08-996-338-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-08-991-944-1  
; Sequence 1, Application US/08991944  
; Patent No. 6280955  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Zhaoan  
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,  
; TITLE OF INVENTION: Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94010  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,944  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 343-4341  
; TELEFAX: (650) 343-4342  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1740 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 10..1719  
; US-08-991-944-1

Query Match 67.3%; Score 1388.4; DB 3; Length 1740;  
Best Local Similarity 89.6%; Pred. No. 0;  
Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

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QY 10 ATGACACTTCTGTGGTGTGTAGTGTCTCTACTTTATGGAACTCTGCAAAAGTGATGCC 69  
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QY 61 TCAGAACGCTGGGATGACCTGGGGACTAGACACATGAGGCAAAATCAAGTGTGTTGAAGAT 120  
DB |||||  
QY 70 TCAGAACGCTGGGATGACCTGGGGACTAGACACATGAGGCAAAATCAAGTGTGTTGAAGAT 129  
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QY 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTGAACACTCTTGAATTTCAACTACAGCACA 180  
DB |||||  
QY 130 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTGAACACTCTTGAATTTCAACTACAGCACA 189  
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QY 181 GCCCAATTCAGCTGGCCCTTACTCTGTATCTGGTATTTGGACTAGGACGACCGGACCTTTGAG 240  
DB |||||  
QY 190 GCCCAATTCAGCTGGCCCTTACTCTGTATCTGGTATTTGGACTAGGACGACCGGACCTTTGAG 249  
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QY 250 GAGCCAAATTAACCTTCGCGCTCCCGAGAAACCGCATTTAGTAAAGGAGAAAGATGTGCTGTGG 309  
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QY 661 CGTACGTTTCACTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720  
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QY 1021 GTTGCCAAAGCAGCAAGGTGAAGCAAGAAAGTCCAGCTCCAGATACACAGTGGAACTG 1080  
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QY 1030 GTTGCCAAAGCAGCAAGGTGAAGCAAGAAAGTCCAGCTCCAGATACACAGTGGAACTG 1089  
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QY 1081 GCTTGTGGTTTTGGAGCCACAGTCTCTGTAGTGTGATTTCTCATTTGTTTACCATGTT 1140  
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QY 1150 TACTGGCTAGAGATGGTCTCTATTTTACCGGGCTCATTTTGGAAACAGATGAACCAATTTA 1209  
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QY 1321 GACCAGACAGTCTCCCTGGGGAAATACAGTGGGAAGCAATTTTGTATTCATTCAATCAGAGA 1380  
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QY 1441 CTGAGTTTAAACTGGGTGTCAATGTGSCCAGAACTCCATTTG---CCACCAAGCTCATTTGTG 1497  
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QY 1450 CTGAGCTCAAGGCTGGCTAGAAAATATGGCTCTCGGGGCAACATCAACGCTCATTTTA 1509  
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RESULT 2

US-09-949-016-313  
; Sequence 313, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 313  
; LENGTH: 4724  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-313

Query Match 67.3%; Score 1388.4; DB 3; Length 4724;  
Best Local Similarity 89.6%; Pred. No. 0; Mismatches 171; Indels 6; Gaps 2;  
Matches 1517; Conservative 0

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DB 207 ATGACACTTCTGTGTGTAGTGAAGTCTCTACTCTTTATGGAATCCTGCAAGTGATGCC 266  
QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCAATGAGGCAATCCAAAGTGTGTAAGAT 120  
DB 267 TCAGAACGCTGCGATGACTGGGACTAGACACCAATGAGGCAATCCAAAGTGTGTAAGAT 326  
QY 121 GAGCCAGCTCGCATCAAGTGCCTCTTTTGAACACCTCTTGAATTCACACTACAGACA 180  
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DB 387 GCCCATTCAAGTGCCTCTCTGATCTGGTATTTGGAAGTGGAGGACCCGGACCTTGAG 446  
QY 241 GAGCCAAATTAATTCGCGCTCCCGAAGCCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300  
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QY 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTTAAGGAACACTACA 360  
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QY 421 CCCATGAACCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480  
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QY 481 CCAAAATGATAGTAAATTTTCCCTCCAGTGTCAAAACGCACTATCACTTGGTATATGGGC 540  
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QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAATTTGAGTTTCCCT 600  
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QY 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720  
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QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780  
DB 927 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 986  
QY 781 GAGCTACTCATTCCTGTACGGTCTATTTTGTGTTTCTGATGGATTTCCGCAATGAGTTT 840  
DB 987 GAGCTACTCATTCCTGTACGGTCTATTTTGTGTTTCTGATGGATTTCCGCAATGAGTTT 1046  
QY 841 TGGTGACCAATTGATCGAAAACCTGTGATGATCATCACTATTGATGTCCACCTTAACGAA 900  
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DB 1107 AGTATAAGTCATAGTAAAGACAGAAAGTGAACAAAGAACTCAGATTTTGTAGCAATCAAGAAA 1166  
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QY 1021 GTTGCCAAAGCGCAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
DB 1227 GTTGCCAAAGCGCAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1286

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QY 1201 GATGGAAAAGAGTATGATATTTATGTATCTTATGCAAGGAATCGGGAAGAGAAATTT 1260  
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QY 1321 GACCGAGACAGTCTGCTGGGGGAAATACAGTGGAAAGCACTTTTGAATTCATTCAGAGA 1380  
DB 1527 GACCGAGACAGTCTGCTGGGGGAAATTTGTACAGATGAGACTTTTGAGCTTCATTCAGAAA 1586  
QY 1381 AGCAGAGGATGATTTGTTCTGAGCCCTGACTATGTGACAGAAAAGACATCAGCATG 1440  
DB 1587 AGCAGAGGATGATTTGTTCTGAGCCCTGACTATGTGAGCCCTGACTATGTGAGCCCTC 1646  
QY 1441 CTGGAGTTTAAACTGGGTGTCTATGTCAGAACTCCATTTG---CCACCAAGCTCATTTGTG 1497  
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QY 1675 TGTCTTTCCAGTC 1688  
DB 1887 GGCCTCTCGTATTC 1900

RESULT 3

US-09-949-016-5448  
; Sequence 5448, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5448  
; LENGTH: 4726  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5448

Query Match 67.3%; Score 1388.4; DB 3; Length 4726;  
Best Local Similarity 89.6%; Pred. No. 0;  
Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

QY 1 ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTATGGAACTCTGCAAGTGAATGCC 60  
DB |||||  
QY 207 ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTATGGAACTCTGCAAGTGAATGCC 266  
DB |||||  
QY 61 TCAGAACGCTGGATGACTGGGGAATGACACATAGGCAAAATCAAGTGTGGAAGAT 120  
DB |||||  
QY 267 TCAGAACGCTGGATGACTGGGGAATGACACATAGGCAAAATCAAGTGTGGAAGAT 326  
DB |||||  
QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTCTGAAATCAACTACAGCACA 180  
DB |||||  
QY 327 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTCTGAAATCAACTACAGCACA 386  
DB |||||  
QY 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTTAGTCTAGCAGGACCGGACCTTGAG 240  
DB |||||  
QY 387 GCCCATTCAGCTGGCCCTTACTCTGATCTGTTATGGAATGGAAGACCGGACCTTGAG 446  
DB |||||  
QY 241 GAGCAATTAATCTCGCCCTCCCGAGAACCGCATTTAGTAAGGAAAGATGTGCTGGG 300  
DB |||||  
QY 447 GAGCAATTAATCTCGCCCTCCCGAGAACCGCATTTAGTAAGGAAAGATGTGCTGGG 506  
DB |||||  
QY 301 TTCGGCCCACTCTCTCAATGACACTGGCACTATACCTGATGTTAAGGAACACTACA 360  
DB |||||  
QY 507 TTCGGCCCACTCTCTCAATGACACTGGCACTATACCTGATGTTAAGGAACACTACA 566  
DB |||||  
QY 361 TATTGAGCAAAAGTTGCAATTCCTTTGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 420  
DB |||||  
QY 567 TATTGAGCAAAAGTTGCAATTCCTTTGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 626  
DB |||||  
QY 421 CCATGAAACTCCAGTGCATTAATCTGATATAGATATGGAATGGAATGCACTTGT 480  
DB |||||  
QY 627 CCATGAAACTCCAGTGCATTAATCTGATATAGATATGGAATGGAATGCACTTGT 686  
DB |||||  
QY 481 CCAATGTAGATGATATTTCTTCCAGTGTCAACCGACTATCACTGTTGATATGGC 540  
DB |||||  
QY 687 CCAATGTAGATGATATTTCTTCCAGTGTCAACCGACTATCACTGTTGATATGGC 746  
DB |||||  
QY 541 TGTATATAAATACAGAAATTTTAAATGTAATACCGAAGGTATGAACCTTGATTTCTTC 600  
DB |||||  
QY 747 TGTATATAAATACAGAAATTTTAAATGTAATACCGAAGGTATGAACCTTGATTTCTTC 806  
DB |||||  
QY 601 ATTGCTTAAATTTCAAAATGGAATTAACATGTTGTTTACATATCCAGAAATGGA 660  
DB |||||  
QY 807 ATTGCTTAAATTTCAAAATGGAATTAACATGTTGTTTACATATCCAGAAATGGA 866  
DB |||||  
QY 661 CGTACGTTTCACTCAACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAATAATGCA 720  
DB |||||  
QY 867 CGTACGTTTCACTCAACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAATAATGCA 926  
DB |||||  
QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780  
DB |||||  
QY 927 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 986  
DB |||||  
QY 781 GAGTACTCAATTCCTGTACGGTCTATTTTATGTTTCTGATGGATTCGCAATGAGTT 840  
DB |||||  
QY 987 GAGTACTCAATTCCTGTACGGTCTATTTTATGTTTCTGATGGATTCGCAATGAGTT 1046  
DB |||||  
QY 841 TGGTGCACATTTGATGGAAGAAACCTGATGATCATCACTATTGATGTCACCAATTAACGA 900  
DB |||||  
QY 1047 TGGTGCACATTTGATGGAAGAAACCTGATGATCATCACTATTGATGTCACCAATTAACGA 1106  
DB |||||  
QY 901 AGTATAAGTCATAGTAGAACAGAAATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960  
DB |||||  
QY 1107 AGTATAAGTCATAGTAGAACAGAAATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1166  
DB |||||  
QY 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGTTCTGTCATGCTAGAGTGCACCAAGCGAA 1020  
DB |||||  
QY 1167 GTTACCTCTGAGGATCTCAAGCGAGCTATGTTCTGTCATGCTAGAGTGCACCAAGCGAA 1226  
DB |||||  
QY 1021 GTTGCAAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGAACCTG 1080  
DB |||||  
QY 1227 GTTGCAAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGAACCTG 1286  
DB |||||

QY 1081 GCTTGTGGTTTTGGAGCCACAGTCTCTGTAGTGGTGAATCTCAATGTTGTTTACCATGTT 1140  
DB |||||  
QY 1287 GCTTGTGGTTTTGGAGCCACAGTCTCTGTAGTGGTGAATCTCAATGTTGTTTACCATGTT 1346  
DB |||||  
QY 1141 TACTGGCTAGAGATGGTCTTATTTTACCGGGCTCAATTTTGGAAACAGATGAACCAATTTA 1200  
DB |||||  
QY 1347 TACTGGCTAGAGATGGTCTTATTTTACCGGGCTCAATTTTGGAAACAGATGAACCAATTTA 1406  
DB |||||  
QY 1201 GATGAAAGAGATGATATTTATGATCTATGCAAGGAATGCGGAAGAAAGAAATTT 1260  
DB |||||  
QY 1407 GATGAAAGAGATGATATTTATGATCTATGCAAGGAATGCGGAAGAAAGAAATTT 1466  
DB |||||  
QY 1261 GTATTACTGACCCCTCCGTGGAGTTTTGGAGAAATGAATTTGGATACAAAGCTGTGCATCTTT 1320  
DB |||||  
QY 1467 GTATTACTGACCCCTCCGTGGAGTTTTGGAGAAATGAATTTGGATACAAAGCTGTGCATCTTT 1526  
DB |||||  
QY 1321 GACCAGACAGTCTGCTGGGGGAAATACAGTGGGAAGCAATTTTGTATTTCAATTCAGAGA 1380  
DB |||||  
QY 1527 GACCAGACAGTCTGCTGGGGGAAATGTCACAGATGAGACTTTGAGCTTCAATTCAGAAA 1586  
DB |||||  
QY 1381 AGCAGAGGATGATTTGTTTCTGAGCCCTGACTATGTGACAGAAAAGAGCATCAGCATG 1440  
DB |||||  
QY 1587 AGCAGAGCCTCTGTTGTTCTTAAGCCCAACTAGTGTCTCCAGGGAACCCAGCCCTC 1646  
DB |||||  
QY 1441 CTGGAGTTTAAACTGGGTGCATGTGCCAGAACTCCATTTG---CCACCAAGCTCATTTGTG 1497  
DB |||||  
QY 1647 CTGGAGCTCAAGGCTGGCTAGAAAATATGGCTCTCGGGGCAACATCAACGTCAATTTTA 1706  
DB |||||  
QY 1498 GTTGAATACCTCCCTTGGACACCCGACCCAGGCATCTTCAGTCAAGAGTCTGTG 1557  
DB |||||  
QY 1707 GTACAGTCAAAAGCTGTGAAGGAAACGAAGGTGAAAGAGCTGAAGAGGCTAAGCGGTG 1766  
DB |||||  
QY 1558 ---TCCTTTGTGAGCTGGAAGGAGAAAGTCCAAACATTTCTGGCTCTATAATTTCTGAAA 1614  
DB |||||  
QY 1767 CTCAGGCTCAATTAATGGAAGGGGAAATCCAAAGTATCCACAGGCGAGTTCTGGAAG 1826  
DB |||||  
QY 1615 GCTTTGCGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGCAGTTCCTGGCTGGAATGAGAGC 1674  
DB |||||  
QY 1827 CAGCTCAGGTTGGCCATGCCAGTGAAGAAAGTCCCGCGGTCTAGCAGTGTATGAGCAG 1886  
DB |||||  
QY 1675 TGCTCTCCAGTC 1688  
DB |||||  
QY 1887 GGCCTCTCGTATTC 1900  
DB |||||

## RESULT 4

US-10-282-162-39  
; Sequence 39, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 39  
; LENGTH: 2703  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-282-162-39

Query Match 52.0%; Score 1073; DB 3; Length 2703;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAACTCTGCAAGTGAATGCC 60

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|||||
1 ATGGTCTCTGTGTGTGTAGTGCTCTACTTTATGGAATCTGCAAGTGATGCC 60
61 TCAGAACGCTGCGATGACTGGGAGTAGACACCATGAGGCAAAATCCAAAGTGTGAAGAT 120
61 TCAGAACGCTGCGATGACTGGGAGTAGACACCATGAGGCAAAATCCAAAGTGTGAAGAT 120
121 GAGCGAGCTCGCATCAAGTGCACCTTTTGAACACTCTTTGAAATTTCAACTACAGCACA 180
121 GAGCGAGCTCGCATCAAGTGCACCTTTTGAACACTCTTTGAAATTTCAACTACAGCACA 180
181 GCCCATTGAGTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
181 GCCCATTGAGTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGCTGTGG 300
241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGCTGTGG 300
301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
361 TATTGCAAGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
361 TATTGCAAGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
421 CCATGAAACTCCAGTGCAATAACTGTAATAGAAATATGGCAATTCAGAGGATCACTTGT 480
421 CCATGAAACTCCAGTGCAATAACTGTAATAGAAATATGGCAATTCAGAGGATCACTTGT 480
481 CCAATGTAGATGGATATTTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 540
481 CCAATGTAGATGGATATTTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 540
541 TGTATATAAATACAGAAATTTTAAATGTAATACCGAAGGTATGAACCTTGAGTTTCCCT 600
541 TGTATATAAATACAGAAATTTTAAATGTAATACCGAAGGTATGAACCTTGAGTTTCCCT 600
601 ATGGCTTAAATTTCAAAATATGAAATTTACACATGTTGTTTACATATCCAGAAATGGA 660
601 ATGGCTTAAATTTCAAAATATGAAATTTACACATGTTGTTTACATATCCAGAAATGGA 660
661 CGTACGTTTCACTCCACGAGCTCTGACTGTAAGGTAGTAGGCTCTCCAAATGCA 720
661 CGTACGTTTCACTCCACGAGCTCTGACTGTAAGGTAGTAGGCTCTCCAAATGCA 720
721 GTGCCCCCTGTGATCCATTCACTCAATGATCATGTTGTTTATGAGAAAGAACCCAGGAG 780
721 GTGCCCCCTGTGATCCATTCACTCAATGATCATGTTGTTTATGAGAAAGAACCCAGGAG 780
781 GAGCTACTCAATCCCTGTACGGTCTATTTTAGTTTTCTGATGATTTCTCGCAATGAGTT 840
781 GAGCTACTCAATCCCTGTACGGTCTATTTTAGTTTTCTGATGATTTCTCGCAATGAGTT 840
841 TGTGTGACCATTCATGGAAGAAACCTGATGACACTATTTGATGCTCACCATTACAGAA 900
841 TGTGTGACCATTCATGGAAGAAACCTGATGACACTATTTGATGCTCACCATTACAGAA 900
901 AGTATAAGTCATAGTAGAAGAGATGAAACCAAGAACTCAGATTTTGGAGCATCAAGAAA 960
901 AGTATAAGTCATAGTAGAAGAGATGAAACCAAGAACTCAGATTTTGGAGCATCAAGAAA 960
961 GTTACCTCTGAGATCTCAAGCGCAGTATGCTGTCTGCTAGTAGAAGTGCCAAAGCGGAA 1020
961 GTTACCTCTGAGATCTCAAGCGCAGTATGCTGTCTGCTAGTAGAAGTGCCAAAGCGGAA 1020
1021 GTTGCCAAAGCAGCCAGGTGAGCAAGTGCAGCTCCAGCTCCAGATACACAGTGGAACTG 1080
1021 GTTGCCAAAGCAGCCAGGTGAGCAAGTGCAGCTCCAGCTCCAGATACACAGTGGAACTG 1080
1081 GCTTGTGGTTTTGGAGCCACAGTCTCTGCTAGTG 1113
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Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTTAGTG 1113

RESULT 5
US-10-282-162-41
; Sequence 41, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-41

Query Match 52.0%; Score 1073; DB 3; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
Db 1 ATGGTGCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
QY 61 TCAGAACGCTGCGATGACTGGGAGTAGACACCATGAGGCAAAATCCAAAGTGTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACTGGGAGTAGACACCATGAGGCAAAATCCAAAGTGTGAAGAT 120
QY 121 GAGCGAGCTCGCATCAAGTGCACCTTTTGAACACTCTTTGAAATTTCAACTACAGCACA 180
Db 121 GAGCGAGCTCGCATCAAGTGCACCTTTTGAACACTCTTTGAAATTTCAACTACAGCACA 180
QY 181 GCCCATTGAGTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
Db 181 GCCCATTGAGTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGCTGTGG 300
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGCTGTGG 300
QY 301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
Db 301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
QY 361 TATTGCAAGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGCAAGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
QY 421 CCATGAAACTCCAGTGCAATAACTGTAATAGAAATATGGCAATTCAGAGGATCACTTGT 480
Db 421 CCATGAAACTCCAGTGCAATAACTGTAATAGAAATATGGCAATTCAGAGGATCACTTGT 480
QY 481 CCAATGTAGATGGATATTTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 540
Db 481 CCAATGTAGATGGATATTTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 540
QY 541 TGTATATAAATACAGAAATTTTAAATGTAATACCGAAGGTATGAACCTTGAGTTTCCCT 600
Db 541 TGTATATAAATACAGAAATTTTAAATGTAATACCGAAGGTATGAACCTTGAGTTTCCCT 600
QY 601 ATGGCTTAAATTTCAAAATATGAAATTTACACATGTTGTTTACATATCCAGAAATGGA 660
Db 601 ATGGCTTAAATTTCAAAATATGAAATTTACACATGTTGTTTACATATCCAGAAATGGA 660
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; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-51

Query Match      51.8%; Score 1069.6; DB 3; Length 2748;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGACACTTCTGTGGTGTAGTGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60
Db |||
Qy 1 ATGGTGCTTCTGTGGTGTAGTGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60
Db |||
Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 120
Db |||
Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 120
Db |||
Qy 121 GAGCCAGCTGCGATCAAGTCCCACTCTTTGAAACCTTTTGAATTAACACTACAGCACA 180
Db |||
Qy 121 GAGCCAGCTGCGATCAAGTCCCACTCTTTGAAACCTTTTGAATTAACACTACAGCACA 180
Db |||
Qy 181 GCCATTACAGCTGGCCCTTACTCTGTATCTGTATTTGAGTACGACGAGCCGGACCTTGAG 240
Db |||
Qy 181 GCCATTACAGCTGGCCCTTACTCTGTATCTGTATTTGAGTACGACGAGCCGGACCTTGAG 240
Db |||
Qy 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300
Db |||
Qy 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300
Db |||
Qy 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTAAGGAACTACATA 360
Db |||
Qy 361 TATTGAGCAAACTTGCATTTCCCTTGGAGTGTTCNAAGACACAGCTGTTTCAATTC 420
Db |||
Qy 361 TATTGAGCAAACTTGCATTTCCCTTGGAGTGTTCNAAGACACAGCTGTTTCAATTC 420
Db |||
Qy 421 CCCATGAATCCCAAGTGCAATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
Db |||
Qy 421 CCCATGAATCCCAAGTGCAATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
Db |||
Qy 481 CCAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGCAATATCACTTGGTATATGGGC 540
Db |||
Qy 481 CCAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGCAATATCACTTGGTATATGGGC 540
Db |||
Qy 541 TGTATTAATACAGAAATTTAATATATGTAATACCGAAGGTATGAACTTGAATTTCCCTC 600
Db |||
Qy 541 TGTATTAATACAGAAATTTAATATATGTAATACCGAAGGTATGAACTTGAATTTCCCTC 600
Db |||
Qy 601 ATTGCCTTAATTTCAAAATATGAAATTAACATATGTTTGTATACATATCCAGAAATGGA 660
Db |||
Qy 601 ATTGCCTTAATTTCAAAATATGAAATTAACATATGTTTGTATACATATCCAGAAATGGA 660
Db |||
Qy 661 CGTACGTTTCATCTCAACAGGACTGTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720
Db |||
Qy 661 CGTACGTTTCATCTCAACAGGACTGTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720
Db |||
Qy 721 GTGCCCCCTGTGATCCATTTCACTTAATGATCATGTGGTCTATGAGAAAGAACAGGAG 780
Db |||
Qy 721 GTGCCCCCTGTGATCCATTTCACTTAATGATCATGTGGTCTATGAGAAAGAACAGGAG 780
Db |||
Qy 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTGTCTGATGGATTTCTCGCAATGAGTT 840
Db |||
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781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTGTCTCGCAATGAGTT 840
Qy 841 TGGTGACCACTTGTATGGAATAAAACCTGTATGATGACATCACTATTGATGTCACATTAACGAA 900
Db |||
Qy 841 TGGTGACCACTTGTATGGAATAAAACCTGTATGATGACATCACTATTGATGTCACATTAACGAA 900
Db |||
Qy 901 AGTATAAGTATAGTATGAAACAGAAAGATGAAACAAAGAACTCAGATTTTGAGCATCAAGAAA 960
Db |||
Qy 901 AGTATAAGTATAGTATGAAACAGAAAGATGAAACAAAGAACTCAGATTTTGAGCATCAAGAAA 960
Db |||
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGTCATGCTAGAAAGTGCAAAAGGCGAA 1020
Db |||
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGTCATGCTAGAAAGTGCAAAAGGCGAA 1020
Db |||
Qy 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGA 1076
Db |||
Qy 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGA 1076
Db |||

RESULT 8
US-10-282-162-53
; Sequence 53, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-53

Query Match      51.8%; Score 1069.6; DB 3; Length 2754;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGACACTTCTGTGGTGTAGTGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60
Db |||
Qy 1 ATGGTGCTTCTGTGGTGTAGTGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60
Db |||
Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 120
Db |||
Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 120
Db |||
Qy 121 GAGCCAGCTGCGATCAAGTCCCACTCTTTGAAACCTTTTGAATTAACACTACAGCACA 180
Db |||
Qy 121 GAGCCAGCTGCGATCAAGTCCCACTCTTTGAAACCTTTTGAATTAACACTACAGCACA 180
Db |||
Qy 181 GCCATTACAGCTGGCCCTTACTCTGTATCTGTATTTGAGTACGACGAGCCGGACCTTGAG 240
Db |||
Qy 181 GCCATTACAGCTGGCCCTTACTCTGTATCTGTATTTGAGTACGACGAGCCGGACCTTGAG 240
Db |||
Qy 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300
Db |||
Qy 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300
Db |||
Qy 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTAAGGAACTACATA 360
Db |||
Qy 361 TATTGAGCAAACTTGCATTTCCCTTGGAGTGTTCNAAGACACAGCTGTTTCAATTC 420
Db |||
Qy 361 TATTGAGCAAACTTGCATTTCCCTTGGAGTGTTCNAAGACACAGCTGTTTCAATTC 420
Db |||
Qy 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTGTCTGATGGATTTCTCGCAATGAGTT 840
Db |||
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421 CCATGAACTCCAGTGCATAAATCTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480  
 Db |||||  
 421 CCATGAACTCCAGTGCATAAATCTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480  
 Qy |||||  
 481 CAAATGTAGATGATATTTCTTCCAGTGTCAAACCGACTATCACTTTGGTATATGGGC 540  
 Db |||||  
 481 CAAATGTAGATGATATTTCTTCCAGTGTCAAACCGACTATCACTTTGGTATATGGGC 540  
 Qy |||||  
 541 TGTATAAATACAGAAATTTAATATGAATTAATACCGAAGGTATGAATTTCTTC 600  
 Db |||||  
 541 TGTATAAATACAGAAATTTAATATGAATTAATACCGAAGGTATGAATTTCTTC 600  
 Qy |||||  
 601 ATTGCCTTAATTTCAAAATATGAAATTAACATGTGTTTGTATATCCAGAAATGGA 660  
 Db |||||  
 601 ATTGCCTTAATTTCAAAATATGAAATTAACATGTGTTTGTATATCCAGAAATGGA 660  
 Qy |||||  
 661 CGTACGTTTTCATCTCACAGGACTCTGACTGTAAAGGTATAGTGGCTCTCCAAAAATGCA 720  
 Db |||||  
 661 CGTACGTTTTCATCTCACAGGACTCTGACTGTAAAGGTATAGTGGCTCTCCAAAAATGCA 720  
 Qy |||||  
 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAG 780  
 Db |||||  
 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAG 780  
 Qy |||||  
 781 GAGTACTCATTTCCCTGTACGGTCTATTTTAGTATTTCTGATGATTTCTCGCAATGAGTT 840  
 Db |||||  
 781 GAGTACTCATTTCCCTGTACGGTCTATTTTAGTATTTCTGATGATTTCTCGCAATGAGTT 840  
 Qy |||||  
 841 TGGTGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGAA 900  
 Db |||||  
 841 TGGTGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGAA 900  
 Qy |||||  
 901 AGTATAAGTCATAGTAGAAGACAGAAATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960  
 Db |||||  
 901 AGTATAAGTCATAGTAGAAGACAGAAATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960  
 Qy |||||  
 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCTGTAGAGTGCCTCAAGCGGAA 1020  
 Db |||||  
 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCTGTAGAGTGCCTCAAGCGGAA 1020  
 Qy |||||

RESULT 9  
 US-10-282-162-55  
 ; Sequence 55, Application US/10282162  
 ; Patent No. 6927044  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
 ; FILE REFERENCE: REG 203-B-US  
 ; CURRENT APPLICATION NUMBER: US/10/282,162  
 ; PRIORITY FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: 09/787,835  
 ; PRIOR FILING DATE: 1999-09-22  
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045  
 ; PRIOR FILING DATE: 1999-09-22  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 55  
 ; LENGTH: 2754  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-282-162-55

Query Match 51.8%; Score 1069.6; DB 3; Length 2754;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGACACTTCTGTGTGTAGTGTCTCTACTTTTATGGAAATCCTGCAAAAGTGATGCC 60  
 Db |||||  
 1 ATGATGCTTCTGTGTGTGTAGTGTCTCTACTTTTATGGAAATCCTGCAAAAGTGATGCC 60  
 Qy 61 TCAGAACGCTGGGATGACTGGGGACTAGACACCATAGAGCAAAATCAAGTGTGTAAGAT 120  
 Db |||||  
 61 TCAGAACGCTGGGATGACTGGGGACTAGACACCATAGAGCAAAATCAAGTGTGTAAGAT 120  
 Qy 121 GAGCCAGCTCCGATCAAGTGGCCACTTTTGAACACTCTTGTGAAATTTCAACTACAGCACA 180  
 Db |||||  
 121 GAGCCAGCTCCGATCAAGTGGCCACTTTTGAACACTCTTGTGAAATTTCAACTACAGCACA 180  
 Qy 181 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTTAGCATAGGACGAGACCGGACCTTTGAG 240  
 Db |||||  
 181 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTTAGCATAGGACGAGACCGGACCTTTGAG 240  
 Qy 241 GAGCCAAATTAATCTCCGCTCCCGAGAAACCGCATTTAGTAAAGGAGAAAGATGTGCTGTGG 300  
 Db |||||  
 241 GAGCCAAATTAATCTCCGCTCCCGAGAAACCGCATTTAGTAAAGGAGAAAGATGTGCTGTGG 300  
 Qy 301 TTCCGGCCCACTCTCTCAATGACACTGSCAACTATACCTGATGTTAAGGAACTACTACA 360  
 Db |||||  
 301 TTCCGGCCCACTCTCTCAATGACACTGSCAACTATACCTGATGTTAAGGAACTACTACA 360  
 Qy 361 TATTGACAGCAAGTGTGCAATTTCCCTTGGAAAGTGTTCAAAAAGACAGCTGTTTCAATTC 420  
 Db |||||  
 361 TATTGACAGCAAGTGTGCAATTTCCCTTGGAAAGTGTTCAAAAAGACAGCTGTTTCAATTC 420  
 Qy 421 CCATGAAATCTCCAGTGCATATACTGTATATAGAAATTTAGCATTTAGGAGTCACTTGT 480  
 Db |||||  
 421 CCATGAAATCTCCAGTGCATATACTGTATATAGAAATTTAGCATTTAGGAGTCACTTGT 480  
 Qy 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAACCGACTATCACTTTGGTATATGGGC 540  
 Db |||||  
 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAACCGACTATCACTTTGGTATATGGGC 540  
 Qy 541 TGTATAAATACAGAAATTTTAAATATGTAATACCCGAGGTATGAACTTTGATTTTCTCT 600  
 Db |||||  
 541 TGTATAAATACAGAAATTTTAAATATGTAATACCCGAGGTATGAACTTTGATTTTCTCT 600  
 Qy 601 ATTGCTTAAATTTCAAATATGGAATTTACATGTGTTTACATATCCAGAAATGGA 660  
 Db |||||  
 601 ATTGCTTAAATTTCAAATATGGAATTTACATGTGTTTACATATCCAGAAATGGA 660  
 Qy 661 CGTACGTTTCACTCCAGGACTCTGACTGTAAAGGTATAGGCTCTCCAAAAATGCA 720  
 Db |||||  
 661 CGTACGTTTCACTCCAGGACTCTGACTGTAAAGGTATAGGCTCTCCAAAAATGCA 720  
 Qy 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAG 780  
 Db |||||  
 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAG 780  
 Qy 781 GAGTACTCATTTCCCTGTACGGTCTATTTTAGTATTTCTGATGATTTCTCGCAATGAGTT 840  
 Db |||||  
 781 GAGTACTCATTTCCCTGTACGGTCTATTTTAGTATTTCTGATGATTTCTCGCAATGAGTT 840  
 Qy 841 TGGTGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGAA 900  
 Db |||||  
 841 TGGTGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGAA 900  
 Qy 901 AGTATAAGTCATAGTAGAAGACAGAAATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960  
 Db |||||  
 901 AGTATAAGTCATAGTAGAAGACAGAAATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960  
 Qy 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCTGTAGAGTGCCTCAAGCGGAA 1020  
 Db |||||  
 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCTGTAGAGTGCCTCAAGCGGAA 1020  
 Qy 1021 GTTGCAAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGA 1076  
 Db |||||  
 1021 GTTGCAAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGA 1076



## RESULT 10

US-09-313-942-27  
; Sequence 27, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC..  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: AND USING  
; CURRENT APPLICATION NUMBER: US/09/313,942  
; CURRENT FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 2733  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2730)  
US-09-313-942-27

Query Match 51.8%; Score 1069.2; DB 3; Length 2733;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1071; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC	60
DB	1	ATGGTGCTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC	60
QY	61	TCGAGACCTGCGATGATCGGGACCTAGACACCATGAGGCAATCCAAAGTGTGAAGAT	120
DB	61	TCGAGACCTGCGATGATCGGGACCTAGACACCATGAGGCAATCCAAAGTGTGAAGAT	120
QY	121	GAGCCAGCTCGCATCAAGTCCCACTCTTTGGAACACTCTTGAATTTCAACTACACACA	180
DB	121	GAGCCAGCTCGCATCAAGTCCCACTCTTTGGAACACTCTTGAATTTCAACTACACACA	180
QY	181	GCCCAATTCAGCTGGCCTTACTCTGATCTGGTATTGGAATAGGAGGACCGGACCTTGAG	240
DB	181	GCCCAATTCAGCTGGCCTTACTCTGATCTGGTATTGGAATAGGAGGACCGGACCTTGAG	240
QY	241	GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGAGAAAGATGCTGTGG	300
DB	241	GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGAGAAAGATGCTGTGG	300
QY	301	TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAGGACACTACA	360
DB	301	TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAGGACACTACA	360
QY	361	TATTGACGAAAAGTGTGCAATTCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTCC	420
DB	361	TATTGACGAAAAGTGTGCAATTCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTCC	420
QY	421	CCCATGAACCTCCAGTGCATAAATCTGTATATAGAAATATGGCAATCAGAGGATCACTGT	480
DB	421	CCCATGAACCTCCAGTGCATAAATCTGTATATAGAAATATGGCAATCAGAGGATCACTGT	480
QY	481	CCAAATGTAGATGGAATTTTCCCTCCAGTGTCAAAACCGCACTATCACTTGGTATATGGG	540
DB	481	CCAAATGTAGATGGAATTTTCCCTCCAGTGTCAAAACCGCACTATCACTTGGTATATGGG	540
QY	541	TGTTATAAATAACAGAAATTTTAATATGTAATACCCGAAGGTATGAATTTGAGTTTCCCT	600
DB	541	TGTTATAAATAACAGAAATTTTAATATGTAATACCCGAAGGTATGAATTTGAGTTTCCCT	600
QY	601	ATTGCCTTAATTTCAAATTAATGAAATTTACACATGTTGTTTACATATCCAGAAAATGGA	660
DB	601	ATTGCCTTAATTTCAAATTAATGAAATTTACACATGTTGTTTACATATCCAGAAAATGGA	660

QY	661	CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGTAGTAGGCTCTCCAAAAATGCA	720
DB	661	CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGTAGTAGGCTCTCCAAAAATGCA	720
QY	721	GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG	780
DB	721	GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG	780
QY	781	GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGGAATTCGCAATGAGTT	840
DB	781	GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGGAATTCGCAATGAGTT	840
QY	841	TGGTGGACCATTCATGTAAGAAAAACCTGATGACATCACTATTGATGTCACTTAACGAA	900
DB	841	TGGTGGACCATTCATGTAAGAAAAACCTGATGACATCACTATTGATGTCACTTAACGAA	900
QY	901	AGTATAAGTCATAGTAGAACAGAGAATGAACAAAGAACTCAGATTTTGAGCATCAAGAA	960
DB	901	AGTATAAGTCATAGTAGAACAGAGAATGAACAAAGAACTCAGATTTTGAGCATCAAGAA	960
QY	961	GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGCTAGAAAGTGCAAAAGCGAA	1020
DB	961	GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGCTAGAAAGTGCAAAAGCGAA	1020
QY	1021	GTTGCCAAAAGCAGCCAAAGGTGAAGCAGAGAAAGTGCCAGCTCCAAAGATACACAGTG	1074
DB	1021	GTTGCCAAAAGCAGCCAAAGGTGAAGCAGAGAAAGTGCCAGCTCCAAAGATACACAGTG	1074

## RESULT 11

US-10-282-162-27  
; Sequence 27, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC..  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: AND USING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 2733  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2730)  
US-10-282-162-27

Query Match 51.8%; Score 1069.2; DB 3; Length 2733;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1071; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC	60
DB	1	ATGGTGCTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC	60
QY	61	TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTGAAGAT	120
DB	61	TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTGAAGAT	120
QY	121	GAGCCAGCTCGCATCAAGTGCCTCTTTGAACTCTTCTGAACTTCTCACTACAGACA	180
DB	121	GAGCCAGCTCGCATCAAGTGCCTCTTTGAACTCTTCTGAACTTCTCACTACAGACA	180
QY	181	GCCCAATTCAGCTGGCCTTACTCTGATCTGGTATTGGAATAGGAGGACCGGACCTTGAG	240

[illegible]

361	QY	1AT1GCACAAAGTGCAT11CCCT1GGAG11G11CAAAAAGACAC1G1111CA111C
495	Db	TACTGCACAAAGTTGCATTTTCCCTCGGAAGTTGTTTCAGAGGACAGCTGTTTCAATCT
421	QY	CCCATGAAACTCCCAAGTCGATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT
555	Db	GCCATGAGATTTCCCAAGTGCAACAAGATGTATATTGAACATGGCAATTCATTAAGATCACATGT
481	QY	CCAAATGTPAGATGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTGATATGGGC
615	Db	CCAAATGTPAGCGGATACTTTTCTTCCAGTGTCAAAACCATCGGTCACTTGGTATAGGGGT
541	QY	TGTTTATAAATACAGAATTTTTTAATAATGTAATACCCGAAGGTATGAACCTTGAGTTTCCCTC

RESULT 12  
US-08-991-944-3  
; Sequence 3, Application US/08991944  
; Patent No. 6280955  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Zhaodan  
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,  
; TITLE OF INVENTION: Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH

Db 675 TGTAAGTAAATAGTGGACCTTTTCAATATGTACTACCGAGGGCATGAACCTTGAGCTTTTTC 734  
Qy 601 ATTGCCTTAATTTCAATATATGAAATTAACATGTGTTGTATACATATCCAGAAATGCA 660  
Db 735 ATCCCTTGTGTTTCAATATACGGAATTAACATGTGTTGTATACATATCTGAAACCGGA 794  
Qy 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720  
Db 795 CGTCTCTTTCACCTCACAGGACTGTGACTGTAAAGGTGTTGGCTCACCAAGGATGCA 854  
Qy 721 GTGCCCCCTGTGTATCAATCACTTAATGATCATGTGGTCTATGAGAAAGAACAGAGAG 780  
Db 855 TTGCCACCCAGAGTCTAATCTCCAAATGACCGTGTGTTGTCTATGAGAAAGAACAGAGAG 914  
Qy 781 GAGCTACTCATTCCTGTACGGTCTATTTTGTAGTTTCTGTATGATGATTCGCAATGAGTT 840  
Db 915 GAACTGGTTATTCCTTGCAAGTCTATTTTCAGTTTCATTTATGGACTCCCAATGAGGTC 974  
Qy 841 TGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCCACCATTAACGAA 900  
Db 975 TGTGGACCATTTGATGGAAAAAGCCTGATGAGTCCAGTCCAGATCACTATTATGAA 1034  
Qy 901 AGTATAAGTCATAGTAGAAGCAGAAAGATGAAACAGAACTCAGATTTTGAGCATCAAGAA 960  
Db 1035 AGTGTAAATTTCTTCAACGGAAGATGAAACAGAACTCAGATTTTGAGCATCAAGAA 1094  
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTCCCAAGCGAA 1020  
Db 1095 GTACCCCCGAGGATCTCAGGCGCAACTATGTCTGTCATGCTCGAAATACCAAGGGGAA 1154  
Qy 1021 GTTGCCAAAGCAGCAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGGAACTG 1080  
Db 1155 GCTGACAGGCTGCCAAGGTGAACAGAAAGTACATACCAAGGTACACAGTAGAATC 1214  
Qy 1081 GCTTGTGGTTTGGAGCCACAGTCCTGTAGTGGTGAATCTCATTTGTTTACCAGTT 1140  
Db 1215 GCCTGTGGTTTGGAGCCACGGTCTTTCTGGTAGTGGTTCTCATTTGGTTTACCAGTT 1274  
Qy 1141 TACTGGCTAGAGATGCTCTATTTTACCGGCTCATTTTGGACAGATGAACCAATTTA 1200  
Db 1275 TACTGGCTAGAGATGCTCTTTTACCGAGCTCACTTTGGAAACAGATGAACCAATTTCT 1334  
Qy 1201 GATGAAAAAGATGATGATATTTATGTATCTTATGCAAGAAATGCGGAAGAAAGAAATTT 1260  
Db 1335 GATGAAAGAGATGATGATATTTATGTTTCTATGCAAGAAATGCGGAAGAAAGAAATTT 1394  
Qy 1261 GTATTAAGTCCCTCGTGGAGTTTGGAGAAATGAAATTTGGATACAAAGCTGTGCATCTTT 1320  
Db 1395 GTGCTGCTGACGCTGCGTGGAGTTTGGAGAAATGAGTTTGGATACAAAGCTGTGCATCTTC 1454  
Qy 1321 GACCGAGACAGTCTGCTGGGGAATACAGTGGAGCAGTATTTGATTTTCAATTCAGAA 1380  
Db 1455 GACAGAGACAGCTGCTGGGGAATTTGTACAGATGAGACCTGAGCTTCATTCAGAA 1514  
Qy 1381 AGCAGAGAGATGATTTGTTCTGAGCCCTGACTATGTGACAGAAAGAGCATGACATG 1440  
Db 1515 AGCAGAGAGTCTGCTGGTGTCTTAAGTCCCACTAGTGTCTCCAGGGAACACAGCCCTC 1574  
Qy 1441 CTGAGTTTAAAGCTGGGTGTATGTGCCAGAACTCCATTTG---CCACCAAGCTCATTTGG 1497  
Db 1575 CTGAGCTCAAGGCTGGCCCTAGAAAAATATGGCTCCCGGGGCAACATCAACGTCATTTTA 1634  
Qy 1498 GTTGAATACCGTCCCTTGGACCCCGCAGGAGTTCCTCAGCTCAAGAGTCTGTG 1557  
Db 1635 GTGCAGTACAAAGCTGTGAAGGACATGAAGGTGAAGAGCTGAAGCGGCTAAGACGGTG 1694  
Qy 1558 ---TCTTTTGTAGCTGGAAGGAGAAAAAGTCCAAACATTTCTGGCTCTAAATCTTGGA 1614  
Db 1695 CTCACGGTCTATTAATGGAAGAGAGAGAAATCCAGTATCTCTCAGGGCAGGTTCTGGAG 1754  
Qy 1615 GCTTTCGGTGTGCTCTTCCCTGA 1639  
Db 1755 CAGTTGAGGCTGGCCATGCCAGTGA 1779

RESULT 13  
US-10-282-162-33  
; Sequence 33, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 2703  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-282-162-33

Query Match 49.3%; Score 1017; DB 3; Length 2703;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTAAGAT 120  
Db 997 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTAAGAT 1056  
Qy 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTTTGAATTTCAACTACAGCACA 180  
Db 1057 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTTTGAATTTCAACTACAGCACA 1116  
Qy 181 GCCAATTCAGCTGGCTTACTCTGATCTGTTATTCGACTAGGACGAGCCGGACCTTGAG 240  
Db 1117 GCCAATTCAGCTGGCTTACTCTGATCTGTTATTCGACTAGGACGAGCCGGACCTTGAG 1176  
Qy 241 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 300  
Db 1177 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 1236  
Qy 301 TTCGGGCCACTCTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360  
Db 1237 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 1296  
Qy 361 TATTGACGCAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420  
Db 1297 TATTGACGCAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 1356  
Qy 421 CCCATGAACCTCCCAAGTGCATAAACTGTATATAGAATATGGCAATTCAGAGGATCACTGT 480  
Db 1357 CCCATGAACCTCCCAAGTGCATAAACTGTATATAGAATATGGCAATTCAGAGGATCACTGT 1416  
Qy 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACGACTATCACTTGGTATATGGGC 540  
Db 1417 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACGACTATCACTTGGTATATGGGC 1476  
Qy 541 TGTATATAAATACAGAAATTTTAATTAATGTAATACCCGGAAGGTATGAACCTTGAGTTTCTTC 600  
Db 1477 TGTATATAAATACAGAAATTTTAATTAATGTAATACCCGGAAGGTATGAACCTTGAGTTTCTTC 1536  
Qy 601 ATTGCTTTAAATTTCAAATTAATGGAATTTACACATGTGTTTGTATATCCAGAAAATGGA 660  
Db 1537 ATTGCTTTAAATTTCAAATTAATGGAATTTACACATGTGTTTGTATATCCAGAAAATGGA 1596  
Qy 661 CGTAGTTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720  
Db 1597 CGTAGTTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 1656

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780  
DB 1657 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716  
QY 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCGCAATGAGTT 840  
DB 1717 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCGCAATGAGTT 1776  
QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCATTATGATGTCCACCATTAACGAA 900  
DB 1777 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCATTATGATGTCCACCATTAACGAA 1836  
QY 901 AGTATAAGTCATAGTAGAACAGAAAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960  
DB 1837 AGTATAAGTCATAGTAGAACAGAAAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1896  
QY 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGCTAGAAAGTCCAAAGCGGAA 1020  
DB 1897 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGCTAGAAAGTCCAAAGCGGAA 1956  
QY 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTCCAGCTCCCAAGATACACAGTGGAA 1077  
DB 1957 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTCCAGCTCCCAAGATACACAGTGGAA 2013

RESULT 14  
US-10-282-162-35  
; Sequence 35, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-282-162-35

Query Match 49.3%; Score 1017; DB 3; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 997 TCAGAACGCTGCGATGACCTGGGGACTAGACACCATGAGGCAATCCAAAGTCTTGAAGAT 1056  
QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTGAACACTTCAACTACAGCACA 180  
DB 1057 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTCTTGAACACTTCAACTACAGCACA 1116  
QY 181 GCGCAATCAGCTGGCTTACTCTGATCTGGTATTTGATAGTACGAGACCGGACCTTGAAG 240  
DB 1117 GCGCAATCAGCTGGCTTACTCTGATCTGGTATTTGATAGTACGAGACCGGACCTTGAAG 1176  
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DB 1177 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTTAGGAGAAAGATGTGCTGTGG 1236  
QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360  
DB 1237 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 1296  
QY 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420

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DB 1357 CCCATGAACCTCCAGTCGATCAAAAAGTCTATATAGAAATATGCAATTCAGAGGATCACTGT 1416  
QY 481 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCCTTTGGTATATGGGC 540  
DB 1417 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCCTTTGGTATATGGGC 1476  
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DB 1957 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTCCAGCTCCCAAGATACACAGTGGAA 2013

RESULT 15  
US-10-282-162-37  
; Sequence 37, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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Query Match 49.3%; Score 1017; DB 3; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1957 GTTGC AAAAGCAGCCAAAGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGGAA 2013  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
9998.826 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1584.6	76.8	2058	6	US-10-061-727-3
3	1388.4	67.3	4724	5	US-10-167-127-9
4	1388.4	67.3	4724	7	US-10-717-597-14
5	1385.2	67.1	1713	5	US-10-215-211-3
6	1075.4	52.1	1077	5	US-10-215-211-5
7	1073	52.0	2703	6	US-10-282-162-39
8	1073	52.0	2703	8	US-10-840-138-9
9	1073	52.0	2703	9	US-10-945-068-9
10	1073	52.0	2703	10	US-11-056-730-9
11	1073	52.0	2703	10	US-11-134-114-39
12	1073	52.0	2709	6	US-10-282-162-41
13	1073	52.0	2709	6	US-10-282-162-43
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16	1073	52.0	2709	9	US-10-945-068-11
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19	1073	52.0	2709	10	US-11-056-730-13
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21	1073	52.0	2709	10	US-11-134-114-43
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23	1069.6	51.8	2748	8	US-10-840-138-21

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26 1069.6 51.8 2748 10 US-11-134-114-51 Sequence 51, Appl  
27 1069.6 51.8 2754 6 US-10-282-162-53 Sequence 53, Appl  
28 1069.6 51.8 2754 8 US-10-840-138-23 Sequence 55, Appl  
29 1069.6 51.8 2754 8 US-10-840-138-23 Sequence 23, Appl  
30 1069.6 51.8 2754 8 US-10-840-138-25 Sequence 23, Appl  
31 1069.6 51.8 2754 9 US-10-945-068-23 Sequence 23, Appl  
32 1069.6 51.8 2754 9 US-10-945-068-25 Sequence 25, Appl  
33 1069.6 51.8 2754 10 US-11-056-730-23 Sequence 23, Appl  
34 1069.6 51.8 2754 10 US-11-056-730-25 Sequence 25, Appl  
35 1069.6 51.8 2754 10 US-11-134-114-53 Sequence 53, Appl  
36 1069.6 51.8 2754 10 US-11-134-114-55 Sequence 55, Appl  
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39 1069.2 51.8 2733 5 US-10-287-035-27 Sequence 27, Appl  
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41 1069.2 51.8 2733 8 US-10-840-138-1 Sequence 1, Appl  
42 1069.2 51.8 2733 9 US-10-945-068-1 Sequence 1, Appl  
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45 1067.4 51.7 3355 6 US-10-205-219-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-10-061-727-1  
; Sequence 1, Application US/10061727  
; Publication No. US20030170632A1  
; GENERAL INFORMATION:  
; APPLICANT: Sims, John E.  
; APPLICANT: Smith, Dirk E.  
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN  
; FILE REFERENCE: 3151-A  
; CURRENT APPLICATION NUMBER: US/10/061,727  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: US 60/244,831  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2064  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2064)  
; OTHER INFORMATION:  
; NAME/KEY: misc\_feature  
; LOCATION: (1792)..(1792)  
; OTHER INFORMATION: "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.

US-10-061-727-1  
Query Match 100.0%; Score 2063; DB 6; Length 2064;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGACACTTCTGTGGTGTAGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC 60  
Db 1 ATGACACTTCTGTGGTGTAGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC 60  
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Qy 1621 CGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGCCAGTTCTGGCTGGAATGAGAGCTGCTCT 1680  
Db 1621 CGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGCCAGTTCTGGCTGGAATGAGAGCTGCTCT 1680  
Qy 1681 TCCAGTCTGACATCAGTCTGGATCAGTTCAAAGGAGGAGAAAGTCTGTTTCAAAGAGGCC 1740  
Db 1681 TCCAGTCTGACATCAGTCTGGATCAGTTCAAAGGAGGAGAAAGTCTGTTTCAAAGAGGCC 1740  
Qy 1741 CCAGAACTTTCAGAGCTCAGAGAGGCTGCAAGTACGCTCCAGGCCCAAGGNCNAATGTCC 1800  
Db 1741 CCAGAACTTTCAGAGCTCAGAGAGGCTGCAAGTACGCTCCAGGCCCAAGGNCNAATGTCC 1800  
Qy 1801 AAGCACCGAGGAGTCTCCGCACTGCGCTGTTGTGTCTACCTACTGTGAAGGAGAG 1860  
Db 1801 AAGCACCGAGGAGTCTCCGCACTGCGCTGTTGTGTCTACCTACTGTGAAGGAGAG 1860  
Qy 1861 AATCACTTTAGAAACAGAGCGGCGAGAGATTCTAAACAGCGCCAGTGGGAGACACAC 1920  
Db 1861 AATCACTTTAGAAACAGAGCGGCGAGAGATTCTAAACAGCGCCAGTGGGAGACACAC 1920  
Qy 1921 CTCTGTAAAGCTGTTCCCAAGAGTCAAGAACTCAATGATACAAAATGGCAACAGATTG 1980  
Db 1921 CTCTGTAAAGCTGTTCCCAAGAGTCAAGAACTCAATGATACAAAATGGCAACAGATTG 1980  
Qy 1981 GAAACCCCTGCTCCCGAGATCTCAGCCCTTGTCTTCTCATCATTTTACGGACTATCCCAAT 2040  
Db 1981 GAAACCCCTGCTCCCGAGATCTCAGCCCTTGTCTTCTCATCATTTTACGGACTATCCCAAT 2040  
Qy 2041 AACAAACGACTTTTATATCCTATAA 2064  
Db 2041 AACAAACGACTTTTATATCCTATAA 2064

## RESULT 2

US-10-061-727-3  
; Sequence 3, Application US/10061727  
; Publication No. US20030170632A1  
; GENERAL INFORMATION:  
; APPLICANT: Sims, John E.  
; APPLICANT: Smith, Dirk E.  
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN  
; FILE REFERENCE: 3151-A  
; CURRENT APPLICATION NUMBER: US/10/061,727  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2058  
; TYPE: DNA  
; ORGANISM: Mus musculus





QY 2041 AACACGACTTTTATATCTCTATAA 2064  
 Db 2035 AACAAAGACTTTTATATCTCTATAA 2058

RESULT 3  
 US-10-167-127-9  
 ; Sequence 9, Application US/10167127  
 ; Publication No. US20030100031A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DOWER, STEVEN  
 ; APPLICANT: DUFF, GORDON W.  
 ; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY  
 ; TITLE OF INVENTION: EVENTS  
 ; FILE REFERENCE: MSA-026.01 (20974-2601)  
 ; CURRENT APPLICATION NUMBER: US/10/167,127  
 ; CURRENT FILING DATE: 2002-06-11  
 ; PRIOR APPLICATION NUMBER: 60/297,305  
 ; PRIOR FILING DATE: 2001-06-11  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 4724  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-167-127-9

Query Match 67.3%; Score 1388.4; DB 5; Length 4724;  
 Best Local Similarity 89.8%; Pred. No. 0;  
 Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

QY 1 ATGACACTTCTGGTGTGTAGTGTCTCTACTTTTATGGAACTCTGCAAGTGTATGCC 60  
 Db 207 ATGACACTTCTGGTGTGTAGTGTCTCTACTTTTATGGAACTCTGCAAGTGTATGCC 266

QY 61 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTGTGGAAT 120  
 Db 267 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTGTGGAAT 326

QY 121 GAGCCAGCTCGCATCAAGTGCCTCTTTGACACTTCTTGAATTCAACTACAGCACA 180  
 Db 327 GAGCCAGCTCGCATCAAGTGCCTCTTTGACACTTCTTGAATTCAACTACAGCACA 386

QY 181 GCCCAATTCAGCTGGCCTTACTCTGATCTGGTATTTGAGCTAGGACGACCGGACCTTGAG 240  
 Db 387 GCCCAATTCAGCTGGCCTTACTCTGATCTGGTATTTGAGCTAGGACGACCGGACCTTGAG 446

QY 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGG 300  
 Db 447 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGG 506

QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCAATGTAAGGACACTACA 360  
 Db 507 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCAATGTAAGGACACTACA 566

QY 361 TATTGACGAAAGTGTGCAATTTCCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTC 420  
 Db 567 TATTGACGAAAGTGTGCAATTTCCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTC 626

QY 421 CCATGAAATCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGT 480  
 Db 627 CCATGAAATCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGT 686

QY 481 CCAATGTAGATGGATATTTCCCTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 540  
 Db 687 CCAATGTAGATGGATATTTCCCTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 746

QY 541 TGTATAAATAACAGAAATTTTAAATATGTAATACCCGAGGATGAACTTGAAGTTCCTC 600  
 Db 747 TGTATAAATAACAGAAATTTTAAATATGTAATACCCGAGGATGAACTTGAAGTTCCTC 806

QY 601 ATTCGCTTAATTTCAAATTAATGAAATTTACATGTTGTTTACATATCCAGAAATGGA 660

Db 807 ATTGCTTTAATTTCAAATAATGAAATTAACATGTTGTTTACATATCCAGAAATGGA 866  
 QY 661 CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAAATGCA 720  
 Db 867 CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAAATGCA 926

QY 721 GTGCCCCCTGTGATCAATTCACCTAATGATCAATGTGGTCTATGAGAAAGAACACAGAGAG 780  
 Db 927 GTGCCCCCTGTGATCAATTCACCTAATGATCAATGTGGTCTATGAGAAAGAACACAGAGAG 986

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTCTTTCTGATGGATTTCTCGAATGAGGTT 840  
 Db 987 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTCTTTCTGATGGATTTCTCGAATGAGGTT 1046

QY 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGCTCAACCATTAACGAA 900  
 Db 1047 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGCTCAACCATTAACGAA 1106

QY 901 AGTATAAGTCTATAGTAGAACAGAGATGAAACCAAGAACTCAGATTTTGAGCATCAAGAAA 960  
 Db 1107 AGTATAAGTCTATAGTAGAACAGAGATGAAACCAAGAACTCAGATTTTGAGCATCAAGAAA 1166

QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTGCTAGAAAGTCCAAAGCGGAA 1020  
 Db 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTGCTAGAAAGTCCAAAGCGGAA 1226

QY 1021 GTTGCAAGACAGCAAGGTGAAGCAGAGAAAGTCCAGCTCCCAAGATACACAGTGGAACTG 1080  
 Db 1227 GTTGCAAGACAGCAAGGTGAAGCAGAGAAAGTCCAGCTCCCAAGATACACAGTGGAACTG 1286

QY 1081 GCTTGTGTTTTGGAGCCACAGCTCCTGCTAGTGGTGAATTTCTCATTTGTTTACCATGTT 1140  
 Db 1287 GCTTGTGTTTTGGAGCCACAGCTCCTGCTAGTGGTGAATTTCTCATTTGTTTACCATGTT 1346

QY 1141 TACTGGCTAGAGATGGTCTCTATTTTACCGGGCTCATTTTGGAAACAGATGAAACCATTTTA 1200  
 Db 1347 TACTGGCTAGAGATGGTCTCTATTTTACCGGGCTCATTTTGGAAACAGATGAAACCATTTTA 1406

QY 1201 GATGAAAGAGATGATGATATTTATGCTTATGCAAGGAATGCGGAAGAAAGAAATTT 1260  
 Db 1407 GATGAAAGAGATGATGATATTTATGCTTATGCAAGGAATGCGGAAGAAAGAAATTT 1466

QY 1261 GTATTACTGACCTCCGTGGAGTGTGGAGAAATGAAATTTGGATACAAGCTGTGCATCTTT 1320  
 Db 1467 GTATTACTGACCTCCGTGGAGTGTGGAGAAATGAAATTTGGATACAAGCTGTGCATCTTT 1526

QY 1321 GACCCAGACAGCTGCTGCTGGGGGAAATACAGTGGAGAGAGTGTGATTTTCAATTCAGAGA 1380  
 Db 1527 GACCCAGACAGCTGCTGCTGGGGGAAATGTCACAGATGAGACTTTGAGCTTTCAATTCAGAAA 1586

QY 1381 AGCAGAAAGATGATGTTGTTCTGAGCCCTGACTATGTACAGAAAAAGAGCATCAGCATG 1440  
 Db 1587 AGCAGAGCCTCTGTTGTTCTTAAGCCCAACTAGTGTCTCAGGGAAACCCAGGCCCTC 1646

QY 1441 CTGGAGTTTAAATCTGGGTGTCTATGTGCCAGAACTCCATTTG---CCACCAAGCTCATTTG 1497  
 Db 1647 CTGGAGCTCAAGGCTGGCCTAGAAAATATGGCTCTCGGGGCAACATCAACGCTCATTTTA 1706

QY 1498 GTTGTAGTACCTGCTCCCTTGAGCACCGGCACCCAGGCAATTTCTTCAGCTCAAAGAGTCTGT 1557  
 Db 1707 GTACAGTACAAAGCTGTGGAAGGAAACGAAAGGTGAAAGAGCTGAAGAGGGCTAAGACGGTG 1766

QY 1558 ---TCTTTTGTGAGCTGGAAAGGGAGAAAAGTCCAAACATTTCTGGCTCTTAAATTTCTGAAA 1614  
 Db 1767 CTCAGGCTCATTTAAATGGAAAGGGGAAAATCCNAGTATCCACAGGGCAGGTTCTCGAAG 1826

QY 1615 GCTTTTGGGTTGGCTTCTCCCTCTGAGAGTCTGAGTGGCAGGTTCTGGCTGGAATGAGAGC 1674  
 Db 1827 CAGCTGCAAGTGGCCATGCGCAGTGAAGAAAGTCCCAGGCGGTCTAGCAGTGTATGAGCAG 1886

QY 1675 TGCTCTTCCAGTC 1688  
 Db 1887 GGCCTCTGTATTTC 1900

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RESULT 4
US-10-717-597-14
; Sequence 14, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Irepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-717-597-14

Query Match 67.3%; Score 1388.4; DB 7; Length 4724;
Best Local Similarity 89.6%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

QY 1 ATGACACTCTGTGGTGTGTAGTGTCTACTTTATGGAATCTCTGAAATCTGCAAAAGTGATGCC 60
DB 207 ATGACACTCTGTGGTGTGTAGTGTCTACTTTATGGAATCTCTGCAAAAGTGATGCC 266

QY 61 TCAGAACGTCGCATCAAGTGCCCACTCTTTGAACTCTTTGAACTCAACTACACACA 180
DB 267 TCAGAACGTCGCATCAAGTGCCCACTCTTTGAACTCTTTGAACTCAACTACACACA 326

QY 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACTCTTTGAACTCAACTACACACA 180
DB 327 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACTCTTTGAACTCAACTACACACA 386

QY 181 GCCATTACAGTGGCCTTACTCTGTATCTGTATTTGCACTAGGCAGACCGGACCTTGAG 240
DB 387 GCCATTACAGTGGCCTTACTCTGTATCTGTATTTGCACTAGGCAGACCGGACCTTGAG 446

QY 241 GAGCCAAATTAACTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
DB 447 GAGCCAAATTAACTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 506

QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCACTGTTAAGGAACTACA 360
DB 507 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCACTGTTAAGGAACTACA 566

QY 361 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
DB 567 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 626

QY 421 CCCATGAAGTCCAGTGCATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
DB 627 CCCATGAAGTCCAGTGCATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 686

QY 481 CCAAAATGTAGATGGAATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGTGTATGGGC 540
DB 687 CCAAAATGTAGATGGAATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGTGTATGGGC 746

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAATCTTGAGTTTCCTC 600
DB 747 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAATCTTGAGTTTCCTC 806

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QY 601 ATTGCTTAAATTTCAAATAATGAAATTTACACATGTGTTGTTACATATCCAGAAATGGA 660
DB 807 ATTGCTTAAATTTCAAATAATGAAATTTACACATGTGTTGTTACATATCCAGAAATGGA 866

QY 661 CGTACGTTTTCATCTCACCAAGGACTCTGACTGTAAGGTTAGTAGGCTCTCCAAAAATGCA 720
DB 867 CGTACGTTTTCATCTCACCAAGGACTCTGACTGTAAGGTTAGTAGGCTCTCCAAAAATGCA 926

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACACAGAGAG 780
DB 927 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACACAGAGAG 986

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGATTTCTCGCAATGAGTT 840
DB 987 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGATTTCTCGCAATGAGTT 1046

QY 841 TGGTGGACCATTTGATGGAAAAAACTGATGATCATCATCTATTGATGTCAACATTAACGAA 900
DB 1047 TGGTGGACCATTTGATGGAAAAAACTGATGATCATCATCTATTGATGTCAACATTAACGAA 1106

QY 901 AGTATAAGTCATAGTAGAACAAGATGAAACAAGAACTCAGATTTTGGAGCATCAAGAAA 960
DB 1107 AGTATAAGTCATAGTAGAACAAGATGAAACAAGAACTCAGATTTTGGAGCATCAAGAAA 1166

QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTGTAGAGTCCAAAGCGCAA 1020
DB 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTGTAGAGTCCAAAGCGCAA 1226

QY 1021 GTTGCAAGACCAAGGTGAAGCAGAAAGTCCAGCTCCAAAGATACACAGTGGAACTG 1080
DB 1227 GTTGCAAGACCAAGGTGAAGCAGAAAGTCCAGCTCCAAAGATACACAGTGGAACTG 1286

QY 1081 GCTTGTGTTTTGGAGCCACAGTCTCTGATGTGGTGTCTCATTTGTTGTTTACCATGTT 1140
DB 1287 GCTTGTGTTTTGGAGCCACAGTCTCTGATGTGGTGTCTCATTTGTTGTTTACCATGTT 1346

QY 1141 TACTGGCTAGAGATCGTCTCTATTTTACCGGGCTCATTTTGGAAACAGATCAAAACCATTTTA 1200
DB 1347 TACTGGCTAGAGATCGTCTCTATTTTACCGGGCTCATTTTGGAAACAGATCAAAACCATTTTA 1406

QY 1201 GATGAAAGAGATGATGATTTATGTATCTCTATGCAAGGAATGCGGAAGAAAGAAATTT 1260
DB 1407 GATGAAAGAGATGATGATTTATGTATCTCTATGCAAGGAATGCGGAAGAAAGAAATTT 1466

QY 1261 GTATTACTGACCCCTCGTGAGTTTTGGAGAAATGAAATTTGGATACAAGCTGTGCATCTTT 1320
DB 1467 GTATTACTGACCCCTCGTGAGTTTTGGAGAAATGAAATTTGGATACAAGCTGTGCATCTTT 1526

QY 1321 GACCGAGACAGTCTGCTGGGGGAAATACAGTGGAGCAGTTTTTGTATTTTCATTCAGAGA 1380
DB 1527 GACCGAGACAGTCTGCTGGGGGAAATGTACAGATGAGACTTTTGAGCTTCATTCAGAAA 1586

QY 1381 AGCAGAGGATGATTTGTTCTGAGCCCTCTGATGTGACAGAAAGAAAGCAATTCAGCATG 1440
DB 1587 AGCAGAGGATGATTTGTTCTGAGCCCTCTGATGTGACAGAAAGAAAGCAATTCAGCATG 1646

QY 1441 CTGGAGTTTAACTGGGTGTCAATGTGCGAGAACTCCATTTG---CCACCAAGCTCAATTGG 1497
DB 1647 CTGGAGTTTAACTGGGTGTCAATGTGCGGTCTGCGGGCAACATCAACGCTCATTTTAA 1706

QY 1498 GTTGTAGTACCGTCCCTTTGAGCACCAGCCAGCATTTCTTCAGCTCAAGAGTCTGTG 1557
DB 1707 GTTGTAGTACCGTCCCTTTGAGCACCAGCCAGCATTTCTTCAGCTCAAGAGTCTGTG 1766

QY 1558 ---TCTTTGTGAGCTGGAGGGGAAAGTCCAAACATTTCTGGCTCTAAATTTCTGGAAA 1614
DB 1767 CTCAGGTCATTAATGGAAGGGGAAATCCAAAGTATCCACAGGGCAGGTTCTGGAAAG 1826

QY 1615 GCTTTGCGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGCAGTTCTGGCTGGAAGTCAAGC 1674
DB 1827 GCTTTGCGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGCAGTTCTGGCTGGAAGTCAAGC 1886

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QY 1675 TGCTCTTCCAGTC 1688
Db 1887 GGCCTCTCGTATTC 1900

RESULT 5
US-10-215-211-3
; Sequence 3, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1713)
; OTHER INFORMATION:
US-10-215-211-3

Query Match 67.1%; Score 1385.2; DB 5; Length 1713;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches 173; Indels 6; Gaps 2;

QY 1 ATGACACTCTCTGGTGTAGTGTAGTCTCTACTTTATGGAATCCTGCAAGTATGCC 60
Db 1 ATGACACTCTCTGGTGTAGTGTAGTGTCTACTTTATGGAATCCTGCAAGTATGCC 60

QY 61 TCAGAAACGCTGGGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTTCAGAT 120
Db 61 TCAGAAACGCTGGGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTTCAGAT 120

QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTTGAACACTTCTTGAACACTTCTTGAACACTT 180
Db 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTTGAACACTTCTTGAACACTTCTTGAACACTT 180

QY 181 GCCCATTCAGCTGGGCTTACTCTGATCTGGTATTTGACCTAGCAGGACGGGACCTTGAG 240
Db 181 GCCCATTCAGCTGGGCTTACTCTGATCTGGTATTTGACCTAGCAGGACGGGACCTTGAG 240

QY 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAAGGAGAAAGATGTGCTGG 300
Db 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAAGGAGAAAGATGTGCTGG 300

QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
Db 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360

QY 361 TATTCGACGAAGTGGCATTTCCCTTGGAGTTGTTCAAAAGACAGCTGTTCAATTCC 420
Db 361 TATTCGACGAAGTGGCATTTCCCTTGGAGTTGTTCAAAAGACAGCTGTTCAATTCC 420

QY 421 CCCATGAACCTCCAGTGCATAAACTGTATATAGAAATAGGCAATTCAGAGGATCACTTGT 480
Db 421 CCCATGAACCTCCAGTGCATAAACTGTATATAGAAATAGGCAATTCAGAGGATCACTTGT 480

QY 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGCATATCACTTGGTATATGGC 540
Db 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGCATATCACTTGGTATATGGC 540

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGGATGAACTTGAGTTTCCTC 600
Db 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGGATGAACTTGAGTTTCCTC 600

1601 ATTCCTTTAAATTCAGAAATTAACATATGTGTGTGTACATATCCAGAAATGGA 660
1601 ATTCCTTTAAATTCAGAAATTAACATATGTGTGTGTGTACATATCCAGAAATGGA 660

1661 CGTACGTTTCACTCATCCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720
1661 CGTACGTTTCACTCATCCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720

1721 GTGCCCTCTGTGATCCATTACCTTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
1721 GTGCCCTCTGTGATCCATTACCTTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780

1781 GAGTACTCATTTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGTT 840
1781 GAGTACTCATTTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGTT 840

1841 TGGTGGACCATGATGGAAAAAACCTGATGACATCACTATTTGATGTCCCAATTAACGAA 900
1841 TGGTGGACCATGATGGAAAAAACCTGATGACATCACTATTTGATGTCCCAATTAACGAA 900

1901 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTTCAGCATCAAGAA 960
1901 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTTCAGCATCAAGAA 960

1961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTCCAAAGCGAA 1020
1961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTCCAAAGCGAA 1020

1021 GTTCCAAAGCAGCAAGGTGAAGAGAAAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080
1021 GTTCCAAAGCAGCAAGGTGAAGAGAAAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080

1081 GCTTGTGGTGTGGAGCCACAGTCTCTAGTGTGATTTCTCATTTGTTTACCATCTTT 1140
1081 GCTTGTGGTGTGGAGCCACAGTCTCTAGTGTGATTTCTCATTTGTTTACCATCTTT 1140

1141 TACTGGCTAGAGATGGTCTATTTTACCGGGCTCATTTTGGAAACAGATGAAACCATTTTA 1200
1141 TACTGGCTAGAGATGGTCTATTTTACCGGGCTCATTTTGGAAACAGATGAAACCATTTTA 1200

1201 GATGGAAGAGATGATATTTATGATCTCTATGCAAGAAATGCGGAAGAGAAAGATTT 1260
1201 GATGGAAGAGATGATATTTATGATCTCTATGCAAGAAATGCGGAAGAGAAAGATTT 1260

1261 GTATTACTGACCTCCGTTGGAGTTTGGAGAAATGAAATTTGGATACAACCTGTGCATCTT 1320
1261 GTATTACTGACCTCCGTTGGAGTTTGGAGAAATGAAATTTGGATACAACCTGTGCATCTT 1320

1321 GACCGAGACAGTCTGCTGGGGAAATACAGTGGAAAGCAGTTTGTGATTTTCAATTCAGAGA 1380
1321 GACCGAGACAGTCTGCTGGGGAAATTTGTACAGATGAGACTTTTGAGCTTCAATTCAGAAA 1380

1381 AGCAGAGGATGATTTGTTCTGAGCCTGACTATTTGACAGAAAGAGCATCAGCATG 1440
1381 AGCAGAGGATGATTTGTTCTGAGCCTGACTATTTGACAGAAAGAGCATCAGCATG 1440

1441 CTGGAGTTTAACTGGGTGTCATGTCGCAGAACTCCATTTG---CCACCAAGCTCAATTTG 1497
1441 CTGGAGTTTAACTGGGTGTCATGTCGCAGAACTCCATTTG---CCACCAAGCTCAATTTG 1497

1497 GTTGAGTACCTGCTCCCTTTGAGCACCCGACCCAGGCAATTTCTAGCTCAAAAGAGTCTG 1557
1497 GTTGAGTACCTGCTCCCTTTGAGCACCCGACCCAGGCAATTTCTAGCTCAAAAGAGTCTG 1557

1501 GTACAGTACAAAGCTGTGAGGAAACGAAAGGTGAAAGAGCTGAAGAGGGCTTAAGCGGTG 1560
1501 GTACAGTACAAAGCTGTGAGGAAACGAAAGGTGAAAGAGCTGAAGAGGGCTTAAGCGGTG 1560

1558 ---TCTTTTGTGAGCTGGAAGGAGAAAGTCCAAACATTTCTGGCTCTAAATTTCTGGAAA 1614
1558 ---TCTTTTGTGAGCTGGAAGGAGAAAGTCCAAACATTTCTGGCTCTAAATTTCTGGAAA 1614

1561 CTCAGGCTCATTAATGGAAGGGGAAAAATCCAAAGTATCCACAGGGCAGGTTCTGGAAG 1620
1561 CTCAGGCTCATTAATGGAAGGGGAAAAATCCAAAGTATCCACAGGGCAGGTTCTGGAAG 1620

1615 GCTTTGGGTTGGGCTCTTCCCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1674
1615 GCTTTGGGTTGGGCTCTTCCCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1674

1621 CAGTGCAGGTGGCCATGCCAGTGNAGNAAAGTCCAGGCGGTCTAGCAGTGTAGGAGCAG 1680
1621 CAGTGCAGGTGGCCATGCCAGTGNAGNAAAGTCCAGGCGGTCTAGCAGTGTAGGAGCAG 1680
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QY 1675 TGCTCTTCCAGTC 1688
Db 1681 GGCCTCTCGTATTC 1694

RESULT 6
US-10-215-211-5
; Sequence 5, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1077)
; OTHER INFORMATION:
US-10-215-211-5

Query Match 52.1%; Score 1075.4; DB 5; Length 1077;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGGTGTAGTGTCTCTACTTTATGGAATCTCTGCAAAAGTGATGCC 60
Db 1 ATGACACTTCTGTGGTGTAGTGTCTCTACTTTATGGAATCTCTGCAAAAGTGATGCC 60

QY 61 TCAGAACGCTGCCATGACCTGGGACTAGACACCATGAGCAAAATCAAGTGTGAAGAT 120
Db 61 TCAGAACGCTGCCATGACCTGGGACTAGACACCATGAGCAAAATCAAGTGTGAAGAT 120

QY 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACTCTTTGAAATTTCAACTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACTCTTTGAAATTTCAACTACAGCACA 180

QY 181 GCCCATTCAGCTGGCCTTACTCTGTATTTGACTAGGACGACCGGACCTTGAG 240
Db 181 GCCCATTCAGCTGGCCTTACTCTGTATTTGACTAGGACGACCGGACCTTGAG 240

QY 241 GAGCCAAATTAACCTTCCGCTCCCGGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCAAATTAACCTTCCGCTCCCGGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300

QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCTATTTAAGGAACACTACA 360
Db 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCTATTTAAGGAACACTACA 360

QY 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420

QY 421 CCCATGAATCCCACTGATCAACTGATATAGATATGGCATTTCAAGGATCACTTGT 480
Db 421 CCCATGAATCCCACTGATCAACTGATATAGATATGGCATTTCAAGGATCACTTGT 480

QY 481 CCAATGTAGATGGATATTTTCCCTCCAGTGTCAAAACCGCATCTCACTTGGTATATGGGC 540
Db 481 CCAATGTAGATGGATATTTTCCCTCCAGTGTCAAAACCGCATCTCACTTGGTATATGGGC 540

QY 541 TGTATTAAATAACAGAAATTTTAAATATGTAATACCCGAAGGATGAACCTTGAGTTTCCTC 600
Db 541 TGTATTAAATAACAGAAATTTTAAATATGTAATACCCGAAGGATGAACCTTGAGTTTCCTC 600
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QY 601 ATTGCTTTAATTTCAAATAATGAAATTACACATGTGTTGTTTACATATCCAGAAATGGA 660
Db 601 ATTGCTTTAATTTCAAATAATGAAATTACACATGTGTTGTTTACATATCCAGAAATGGA 660

QY 661 CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAATGCA 720
Db 661 CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAATGCA 720

QY 721 GTGCCCCCTGTGATCGATTCACCTAATGATCATGTGCTCTATGAGAAAGAACACAGAGAG 780
Db 721 GTGCCCCCTGTGATCGATTCACCTAATGATCATGTGCTCTATGAGAAAGAACACAGAGAG 780

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTAGTTTCTGATGATTTCTCGCAATGAGTT 840
Db 781 GAGCTACTCATTTCCCTGTACGGTCTATTTAGTTTCTGATGATTTCTCGCAATGAGTT 840

QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACGAA 900
Db 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACGAA 900

QY 901 AGTATAAGTCATAGTAGAACAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAACAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAA 960

QY 961 GTTACTCTGTAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAAGTCCCAAGGCGAA 1020
Db 961 GTTACTCTGTAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAAGTCCCAAGGCGAA 1020

QY 1021 GTTGCAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGGAA 1077
Db 1021 GTTGCAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGGAA 1077
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## RESULT 7

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US-10-282-162-39
; Sequence 39, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-39
```

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Query Match 52.0%; Score 1073; DB 6; Length 2703;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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QY 1 ATGACACTTCTGTGGTGTAGTGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
Db 1 ATGAGCTTCTGTGGTGTAGTGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60

QY 61 TCAGAACGCTCGCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT 120
Db 61 TCAGAACGCTCGCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT 120

QY 121 GAGCCAGCTCGCATCAAGTGGCCCACTTTTGAAACACTCTTTGAAATTTCAACTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTGGCCCACTCTTTTGAAACACTCTTTGAAATTTCAACTACAGCACA 180
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181 GCCATTACAGTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 240
181 GCCATTACAGTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 240
241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
361 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATCC 420
361 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATCC 420
421 CCCATGAAACTCCAGTGATGATAAAGTATATAGAAATATGGAATATGGAATATGGAAT 480
421 CCCATGAAACTCCAGTGATGATAAAGTATATAGAAATATGGAATATGGAATATGGAAT 480
481 CCAAAATGTAGATGGATATTTTCCCTCCAGTGCAAAACCGACTATCACTTGGTATATGGC 540
481 CCAAAATGTAGATGGATATTTTCCCTCCAGTGCAAAACCGACTATCACTTGGTATATGGC 540
541 TGTATATAAATAACAGAAATTTTAAATATGTAATACCCGAAAGTATGAACTTGGATTTCCCTC 600
541 TGTATATAAATAACAGAAATTTTAAATATGTAATACCCGAAAGTATGAACTTGGATTTCCCTC 600
601 ATTGCTTAAATTTCAAAATATGGAATTTACATGATGTTGTTACATATCCAGAAATGGA 660
601 ATTGCTTAAATTTCAAAATATGGAATTTACATGATGTTGTTACATATCCAGAAATGGA 660
661 CGTAGCTTTCACTCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAATGCA 720
661 CGTAGCTTTCACTCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAATGCA 720
721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
781 GAGCTACTCAATTCCTGTACGCTCTATTTAGTTTCTGATGGATTCGCAATGAGGTT 840
781 GAGCTACTCAATTCCTGTACGCTCTATTTAGTTTCTGATGGATTCGCAATGAGGTT 840
841 TGGTGGACCAATGATGGAAAGAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
841 TGGTGGACCAATGATGGAAAGAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
901 AGTATAAGTCAATGATGAGAACAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960
901 AGTATAAGTCAATGATGAGAACAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960
961 GTTACTCTGAGGATCTCAAGGGAGCTATGCTGTGATGTTCTGATGGATTCGCAATGAGGTT 1020
961 GTTACTCTGAGGATCTCAAGGGAGCTATGCTGTGATGTTCTGATGGATTCGCAATGAGGTT 1020
1021 GTTGCAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCCTCAAGATACACAGTGAAGCTG 1080
1021 GTTGCAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCCTCAAGATACACAGTGAAGCTG 1080
1081 GCTGTGTTTGGAGCCACAGTCTCTGATG 1113
1081 TGCAAGAACGTTGAAGAAATAATTTTAGTG 1113

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RESULT 8

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US-10-840-138-9
; Sequence 9, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
; APPLICANT: Lin, Hsien Chieh
; APPLICANT: Karow, Margaret

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; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840,138
; CURRENT FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-138-9

```

Query Match 52.0%; Score 1073; DB 8; Length 2703;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 1 ATGACATTTCTGTGGTGTAGTGAGTCTCTACTTTTATGGAATCTCTCAAGTGATGCC 60
Db 1 ATGGTGCTTCTGTGGTGTAGTGAGTCTCTACTTTTATGGAATCTCTCAAGTGATGCC 60
Qy 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAATCCAAGTGTTCGAAGAT 120
Db 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAATCCAAGTGTTCGAAGAT 120
Qy 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTTGAACACACTCTTTTGAATTTCAACTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTTGAACACACTCTTTTGAATTTCAACTACAGCACA 180
Qy 181 GCCATTCAGCTGCGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 240
Db 181 GCCATTCAGCTGCGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 240
Qy 241 GAGCCAAATTAATTTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCGTGG 300
Db 241 GAGCCAAATTAATTTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCGTGG 300
Qy 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
Db 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
Qy 361 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTC 420
Db 361 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTC 420
Qy 421 CCCATGAAACTCCAGTGATGATAAAGTATATAGAAATATGGAATATGGAATATGGAAT 480
Db 421 CCCATGAAACTCCAGTGATGATAAAGTATATAGAAATATGGAATATGGAATATGGAAT 480
Qy 481 CCAAAATGTAGATGGATATTTTCCCTCCAGTGCAAAACCGACTATCACTTGGTATATGGC 540
Db 481 CCAAAATGTAGATGGATATTTTCCCTCCAGTGCAAAACCGACTATCACTTGGTATATGGC 540
Qy 541 TGTATATAAATAACAGAAATTTTAAATATGTAATACCCGAAAGTATGAACTTGGATTTCCCTC 600
Db 541 TGTATATAAATAACAGAAATTTTAAATATGTAATACCCGAAAGTATGAACTTGGATTTCCCTC 600
Qy 601 ATTGCTTAAATTTCAAAATATGGAATTTACATGATGTTGTTACATATCCAGAAATGGA 660
Db 601 ATTGCTTAAATTTCAAAATATGGAATTTACATGATGTTGTTACATATCCAGAAATGGA 660
Qy 661 CGTAGCTTTCACTCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAATGCA 720
Db 661 CGTAGCTTTCACTCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
Qy 781 GAGCTACTCAATTCCTGTACGCTCTATTTAGTTTCTGATGGATTCGCAATGAGGTT 840
Db 781 GAGCTACTCAATTCCTGTACGCTCTATTTAGTTTCTGATGGATTCGCAATGAGGTT 840
Qy 841 TGGTGGACCAATGATGGAAAGAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900

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Db 841 TGGTGGACCATTTGATGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAA 1080
Qy 1081 CTTTGTGGTTTGGAGCCACAGTCTGCTAGTG 1113
Db 1081 TGAAGGAACGTGAAGAAAAATAATTTTAGTG 1113

RESULT 9
US-10-945-068-9
; Sequence 9, Application US/10945068
; Publication No. US20050129685A1
; GENERAL INFORMATION:
; APPLICANT: Jingtai Cao
; TITLE OF INVENTION: USE OF IL-1 BLOCKERS TO PREVENT CORNEAL INFLAMMATION
; FILE REFERENCE: REG 2084
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: US/10/945,068
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-945-068-9

Query Match 52.0%; Score 1073; DB 9; Length 2703;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 ATGACACTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAAAGTGATGCC 60
Db 1 ATGGTGCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAAAGTGATGCC 60

Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAATCCAGTGTGTTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAATCCAGTGTGTTGAAGAT 120

Qy 121 GAGCCAGCTCGCATCAAGTGCCACTCTTTGAACACTTTTGAATTTCAACTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTGCCACTCTTTGAACACTTTTGAATTTCAACTACAGCACA 180

Qy 181 GCCATTTCAGCTGGCCCTTACTCTGATCTGTTAGACTAGGAGGAGGACCTTTGAG 240
Db 181 GCCATTTCAGCTGGCCCTTACTCTGATCTGTTAGACTAGGAGGAGGACCTTTGAG 240

Qy 241 GAGCCATTAACTTCCGCTTCCGAGAACCGCATTTAGTAAGAGAGAGATGCTGTGG 300
Db 241 GAGCCATTAACTTCCGCTTCCGAGAACCGCATTTAGTAAGAGAGAGATGCTGTGG 300

Qy 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTTAAGGAACACTACA 360
Db 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTTAAGGAACACTACA 360

Qy 361 TATTGACGAAAGTTGATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Db 361 TATTGACGAAAGTTGATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
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Qy 421 CCCATGAACCTCCAGTGCATAAACTGTATATAGAAATATGGCATTTCAGAGGATCACTTGT 480
Db 421 CCCATGAACCTCCAGTGCATAAACTGTATATAGAAATATGGCATTTCAGAGGATCACTTGT 480
Qy 481 CCAAAATGTAGATGGATATTTTCTCCAGTGTGCAAAACCGACTATCACTTTGGTATATGGGC 540
Db 481 CCAAAATGTAGATGGATATTTTCTCCAGTGTGCAAAACCGACTATCACTTTGGTATATGGGC 540
Qy 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 600
Db 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 600
Qy 601 ATTGCCTTAATTTCAAAATATGGAATTAACATGTTGTTTACATATCCAGAAATATGGA 660
Db 601 ATTGCCTTAATTTCAAAATATGGAATTAACATGTTGTTTACATATCCAGAAATATGGA 660
Qy 661 CGTACGTTTCACTCTCACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATATGCA 720
Db 661 CGTACGTTTCACTCTCACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTCACTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
Db 721 GTGCCCCCTGTGATCCATTCACTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
Qy 781 GAGCTACTCACTTCCCTGTAGGCTCTATTTTAGTTTCTGATGGATTTCTCGCAATGAGTT 840
Db 781 GAGCTACTCACTTCCCTGTAGGCTCTATTTTAGTTTCTGATGGATTTCTCGCAATGAGTT 840
Qy 841 TGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Db 841 TGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGAGTGCCTCAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGAGTGCCTCAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAA 1080
Qy 1081 GCTTGTGGTTTGGAGCCACAGTCTGCTAGTG 1113
Db 1081 TGAAGGAACGTGAAGAAAAATAATTTTAGTG 1113

RESULT 10
US-11-056-730-9
; Sequence 9, Application US/11056730
; Publication No. US20050197293A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Stahl, Neil
; APPLICANT: Radin, Allen
; APPLICANT: Weinstein, Steven
; APPLICANT: Calaprice, Denise
; APPLICANT: Karow, Margaret
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Use of an IL-1 Antagonist for Treating Arthritis
; FILE REFERENCE: 203G
; CURRENT FILING DATE: 2005-02-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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Db 421 CCCATGAACCTCCAGTGCAATAAATCTGTATAGAAATATGCAATTCAGAGGATCACCTGT 480  
Qy 481 CCAATGTAGATGATATTTTCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGC 540  
Db 481 CCAATGTAGATGATATTTTCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGC 540  
Qy 541 TGTATATAAATACAGAAATTTTAATAATGTAAATACCCGAAGGTATGAATTCAGTTTCCTC 600  
Db 541 TGTATATAAATACAGAAATTTTAATAATGTAAATACCCGAAGGTATGAATTCAGTTTCCTC 600  
Qy 601 ATTGCCCTTAATTTCAATAATATGAAATTTACACATGTGTGTATACATATCCAGAAATATGGA 660  
Db 601 ATTGCCCTTAATTTCAATAATATGAAATTTACACATGTGTGTATACATATCCAGAAATATGGA 660  
Qy 661 CGTACGTTTCACTCACAGGACTCTGACTGTAAAGGTATGAGGCTCTCCAAAAAATGCA 720  
Db 661 CGTACGTTTCACTCACAGGACTCTGACTGTAAAGGTATGAGGCTCTCCAAAAAATGCA 720  
Qy 721 GTGCCCCCTGTGATCCCAATTCACCTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780  
Db 721 GTGCCCCCTGTGATCCCAATTCACCTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780  
Qy 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT 840  
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT 840  
Qy 841 TGTGGACCATATGATGAAAAAACCTGATGACATCATATTGATGTACCCATTAAGGAA 900  
Db 841 TGTGGACCATATGATGAAAAAACCTGATGACATCATATTGATGTACCCATTAAGGAA 900  
Qy 901 AGTATAAGTCATAGTAGAACAAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960  
Db 901 AGTATAAGTCATAGTAGAACAAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960  
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGAGTGCACAAAGGCGAA 1020  
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGAGTGCACAAAGGCGAA 1020  
Qy 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGGAAAA 1080  
Db 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGGAAAA 1080  
Qy 1081 GCTTGTGGTTTTGGAGCCACAGTCCTCTAGTG 1113  
Db 1081 TGCAGGAACGTGAAGAAAAAATAATTTTAGTG 1113

RESULT 12  
US-10-282-162-41  
; Sequence 41, Application US/10282162  
; Publication No. US20030143697A1  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 41  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-282-162-41

Query Match 52.0%; Score 1073; DB 6; Length 2709;  
Best Local Similarity 97.8%; Pred. No. 0;

Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
Qy 1 ATGACACTTCTGTGGTGTAGTGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC 60  
Db 1 ATGGTCTTCTGTGGTGTAGTGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC 60  
Qy 61 TCAGAAACGCTGCCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120  
Db 61 TCAGAAACGCTGCCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120  
Qy 121 GAGCCAGCTCGCATCAAGTGGCCCACTCTTTTGAACACTTCTTTGAAATTCAACTACAGCACA 180  
Db 121 GAGCCAGCTCGCATCAAGTGGCCCACTCTTTTGAACACTTCTTTGAAATTCAACTACAGCACA 180  
Qy 181 GCCCATTCAGCTGGCCCTTACTCTGTATCTGGACTAGGACGACCGGACCTTGAG 240  
Db 181 GCCCATTCAGCTGGCCCTTACTCTGTATCTGGACTAGGACGACCGGACCTTGAG 240  
Qy 241 GAGCCAAATTAACCTTCGCGCCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCCTGTGG 300  
Db 241 GAGCCAAATTAACCTTCGCGCCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCCTGTGG 300  
Qy 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTTAAAGAAACACTTACA 360  
Db 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTTAAAGAAACACTTACA 360  
Qy 361 TATTGACGACAAAGTTCGATTTCCCTTTGGAGTTGTTTCAAAAGACAGCTGTTTCAATTC 420  
Db 361 TATTGACGACAAAGTTCGATTTCCCTTTGGAGTTGTTTCAAAAGACAGCTGTTTCAATTC 420  
Qy 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGAATATGGCATTCAGAGGATCACTTGT 480  
Db 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGAATATGGCATTCAGAGGATCACTTGT 480  
Qy 481 CCAAAATGTAGATGGAATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540  
Db 481 CCAAAATGTAGATGGAATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540  
Qy 541 TGTATATAAATACAGAAATTTTAATAATGTAAATACCCGAAGGTATGAATTCAGTTTCCTC 600  
Db 541 TGTATATAAATACAGAAATTTTAATAATGTAAATACCCGAAGGTATGAATTCAGTTTCCTC 600  
Qy 601 ATTGCCCTTAATTTCAATAATATGAAATTTACACATGTGTGTGTACATATCCAGAAATATGGA 660  
Db 601 ATTGCCCTTAATTTCAATAATATGAAATTTACACATGTGTGTGTACATATCCAGAAATATGGA 660  
Qy 661 CGTACGTTTCACTCACAGGACTCTGACTGTAAAGGTATGAGGCTCTCCAAAAAATGCA 720  
Db 661 CGTACGTTTCACTCACAGGACTCTGACTGTAAAGGTATGAGGCTCTCCAAAAAATGCA 720  
Qy 721 GTGCCCCCTGTGATCCCAATTCACCTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780  
Db 721 GTGCCCCCTGTGATCCCAATTCACCTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780  
Qy 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT 840  
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT 840  
Qy 841 TGTGGACCATATGATGAAAAAACCTGATGACATCATATTGATGTACCAATTAAGGAA 900  
Db 841 TGTGGACCATATGATGAAAAAACCTGATGACATCATATTGATGTACCAATTAAGGAA 900  
Qy 901 AGTATAAGTCATAGTAGAACAAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960  
Db 901 AGTATAAGTCATAGTAGAACAAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960  
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGAGTGCACAAAGGCGAA 1020  
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGAGTGCACAAAGGCGAA 1020  
Qy 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080  
Db 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080

```
QY 1081 GCTTGTGGTTTGGAGCCACAGCTCTGCTAGTG 1113
Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTAGTG 1113

RESULT 13
US-10-282-162-43
; Sequence 43, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-43

Query Match 52.0%; Score 1073; DB 6; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGACACTCTGTGGTGTAGTGACTCTACTTTTATGGATCTCTGCAAGTGTATGCC 60
Db 1 ATGGTCTCTGTGGTGTAGTGACTCTACTTTTATGGATCTCTGCAAGTGTATGCC 60

QY 61 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTTTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTTTGAAGAT 120

QY 121 GAGCCAGCTGCGATCAAGTGGCCACTCTTTTGAACACTCTTGAANAATCAACTACAGCACA 180
Db 121 GAGCCAGCTGCGATCAAGTGGCCACTCTTTTGAACACTCTTGAANAATCAACTACAGCACA 180

QY 181 GCCATTTCAGCTGGCCCTTACTCTGTATCTGTATTTGACTAGGCAGGACCGGACCTTGAG 240
Db 181 GCCATTTCAGCTGGCCCTTACTCTGTATCTGTATTTGACTAGGCAGGACCGGACCTTGAG 240

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300

QY 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTATTAAGGAACACTACA 360
Db 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTATTAAGGAACACTACA 360

QY 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTTGTTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTTGTTTCAAAAAGACAGCTGTTTCAATTC 420

QY 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGATAATGCGATTTCAGAGGATCACTTGT 480
Db 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGATAATGCGATTTCAGAGGATCACTTGT 480

QY 481 CCMAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db 481 CCMAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540

QY 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGAATTCCTC 600
Db 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGAATTCCTC 600
```

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QY 601 ATTGCTTTAATTTCAAATAATGAAATTAACACATGTGTTGTTTACATATCCAGAAAAATGGA 660
Db 601 ATTGCTTTAATTTCAAATAATGAAATTAACACATGTGTTGTTTACATATCCAGAAAAATGGA 660

QY 661 CGTAGCTTTTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Db 661 CGTAGCTTTTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720

QY 721 GTGCCCCCTGTGATCACTTACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
Db 721 GTGCCCCCTGTGATCACTTACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780

QY 781 GAGCTACTCACTTCCCTGTACGCTCTATTTTAGTCTTTTCTGATGGATTTCTCGCAATGAGTT 840
Db 781 GAGCTACTCACTTCCCTGTACGCTCTATTTTAGTCTTTTCTGATGGATTTCTCGCAATGAGTT 840

QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACATTAACGAA 900
Db 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACATTAACGAA 900

QY 901 AGTATAAGTTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTGAAGCATCAAGAAA 960
Db 901 AGTATAAGTTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTGAAGCATCAAGAAA 960

QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGTCTAGAGTGCCAAAGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGTCTAGAGTGCCAAAGCGAA 1020

QY 1021 GTTGCCAAAGCAGCCAGGTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCCAAAGCAGCCAGGTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGAACTG 1080

QY 1081 GCTTGTGGTTTGGAGCCACAGCTCTGCTAGTG 1113
Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTAGTG 1113

RESULT 14
US-10-840-138-11
; Sequence 11, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
; APPLICANT: Karow, Margaret
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840,138
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-138-11

Query Match 52.0%; Score 1073; DB 8; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGACACTCTGTGGTGTAGTGACTCTACTTTTATGGAACTCTGCAAAAGTGTATGCC 60
Db 1 ATGGTGTCTTCTGTGTGTAGTGACTCTACTTTTATGGAACTCTGCAAAAGTGTATGCC 60

QY 61 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTGTTTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTGTTTGAAGAT 120

QY 121 GAGCCAGCTGCGATCAAGTGGCCACTCTTTTGAACACTCTTGAANAATCAACTACAGCACA 180
Db 121 GAGCCAGCTGCGATCAAGTGGCCACTCTTTTGAACACTCTTGAANAATCAACTACAGCACA 180

QY 181 GCCATTTCAGCTGGCCCTTACTCTGTATCTGTATTTGACTAGGCAGGACCGGACCTTGAG 240
Db 181 GCCATTTCAGCTGGCCCTTACTCTGTATCTGTATTTGACTAGGCAGGACCGGACCTTGAG 240

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300

QY 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTATTAAGGAACACTACA 360
Db 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTATTAAGGAACACTACA 360

QY 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTTGTTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTTGTTTCAAAAAGACAGCTGTTTCAATTC 420

QY 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGATAATGCGATTTCAGAGGATCACTTGT 480
Db 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGATAATGCGATTTCAGAGGATCACTTGT 480

QY 481 CCMAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db 481 CCMAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540

QY 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGAATTCCTC 600
Db 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGAATTCCTC 600
```

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Qy 181 GCCATTGAGTGGCCCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 240
    |||
Db 181 GCCATTGAGTGGCCCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 240

Qy 241 GAGCAATTAACTTCCGCTCCCGGAAACCGCATTAAGTAAAGGAGAAAGATGCTGTGG 300
    |||
Db 241 GAGCAATTAACTTCCGCTCCCGGAAACCGCATTAAGTAAAGGAGAAAGATGCTGTGG 300

Qy 301 TTCGGGCCACTCTCTCAATGACACTGGCACTATACCTGCACTGTTTAAAGGAAACACTACA 360
    |||
Db 301 TTCGGGCCACTCTCTCAATGACACTGGCACTATACCTGCACTGTTTAAAGGAAACACTACA 360

Qy 361 TATTGACGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
    |||
Db 361 TATTGACGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420

Qy 421 CCCATGAAACTCCAGTGCATTAACCTGTATATAGAAATATGGCAATTCAGAGATCACTTGT 480
    |||
Db 421 CCCATGAAACTCCAGTGCATTAACCTGTATATAGAAATATGGCAATTCAGAGATCACTTGT 480

Qy 481 CCAAACTGTAGATGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
    |||
Db 481 CCAAACTGTAGATGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540

Qy 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAATTTGAGTTTCC 600
    |||
Db 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAATTTGAGTTTCC 600

Qy 601 ATTGCTTAAATTTCAAAATATGGAATTAACAATGTGTTTATCATATTCAGAAAAATGGA 660
    |||
Db 601 ATTGCTTAAATTTCAAAATATGGAATTAACAATGTGTTTATCATATTCAGAAAAATGGA 660

Qy 661 CGTAGCTTTCATCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAAATGCA 720
    |||
Db 661 CGTAGCTTTCATCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAAATGCA 720

Qy 721 GTGCCCCCTGTGATCCATTCACTTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780
    |||
Db 721 GTGCCCCCTGTGATCCATTCACTTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780

Qy 781 GAGCTACTCAATCCCTGTACGGTCTATTTAGTATTTCTGATGGATTCTCGCAATGAGTT 840
    |||
Db 781 GAGCTACTCAATCCCTGTACGGTCTATTTAGTATTTCTGATGGATTCTCGCAATGAGTT 840

Qy 841 TGTGGACCAATTTGATGAAAAAACCCTGATGACATCACTATTGATGTCACCAATTAACGAA 900
    |||
Db 841 TGTGGACCAATTTGATGAAAAAACCCTGATGACATCACTATTGATGTCACCAATTAACGAA 900

Qy 901 AGTATAGTCTATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGACATCAAGAAA 960
    |||
Db 901 AGTATAGTCTATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGACATCAAGAAA 960

Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCACTAGAGAGTCCAAAGGCGAA 1020
    |||
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCACTAGAGAGTCCAAAGGCGAA 1020

Qy 1021 GTTGCCAAAGCAGGCAAGGTGAAGCAAGAGTGGCAGCTCAAGATACACAGTGGAACTG 1080
    |||
Db 1021 GTTGCCAAAGCAGGCAAGGTGAAGCAAGAGTGGCAGCTCAAGATACACAGTGGAACTG 1080

Qy 1081 GCTTGTGTTTGGAGCCACAGTCCCTGCTAGTG 1113
    |||
Db 1081 TGCAGGACGTTGAGNAGAAAAATAATTTTAGTG 1113
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RESULT 15  
US-10-840-138-13  
; Sequence 13, Application US/10840138  
; Publication No. US20040224893A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Li-Hsien  
; APPLICANT: Lin, Hsin Chieh  
; APPLICANT: Karow, Margaret

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia  
; FILE REFERENCE: REG 207A  
; CURRENT APPLICATION NUMBER: US/10/840,138  
; CURRENT FILING DATE: 2004-05-06  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-840-138-13

Query Match 52.0%; Score 1073; DB 8; Length 2709;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```
Qy 1 ATGACACTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
    |||
Db 1 ATGGTGCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60

Qy 61 TCAGAACGCTGCGATGACCTGGGCACTAGACACCATGAGGCAAAATCCAAAGTGTGTTGAAGAT 120
    |||
Db 61 TCAGAACGCTGCGATGACCTGGGCACTAGACACCATGAGGCAAAATCCAAAGTGTGTTGAAGAT 120

Qy 121 GAGCCAGCTCGCATCAAGTGCCTTCTTTGAAACACTTCTTGAATTTCAACTACAGCACA 180
    |||
Db 121 GAGCCAGCTCGCATCAAGTGCCTTCTTTGAAACACTTCTTGAATTTCAACTACAGCACA 180

Qy 181 GCCCATTTAGCTGGCCTTACTCTGATCTGGTATTTGGAATAGGACGACCGGACCTTTGAG 240
    |||
Db 181 GCCCATTTAGCTGGCCTTACTCTGATCTGGTATTTGGAATAGGACGACCGGACCTTTGAG 240

Qy 241 GAGCCAAATTAACCTCCGCTCCCGGAGAACCCGATTTAGTAAAGGAGAAAGATGTCCTGG 300
    |||
Db 241 GAGCCAAATTAACCTCCGCTCCCGGAGAACCCGATTTAGTAAAGGAGAAAGATGTCCTGG 300

Qy 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTTTAAAGGAAACACTACA 360
    |||
Db 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTTTAAAGGAAACACTACA 360

Qy 361 TATTGACGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
    |||
Db 361 TATTGACGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420

Qy 421 CCCATGAAACTCCAGTGCATTAACCTGTATATAGAAATATGGCAATTCAGAGATCACTTGT 480
    |||
Db 421 CCCATGAAACTCCAGTGCATTAACCTGTATATAGAAATATGGCAATTCAGAGATCACTTGT 480

Qy 481 CCAAACTGTAGTGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
    |||
Db 481 CCAAACTGTAGTGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540

Qy 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAATTTGAGTTTCC 600
    |||
Db 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAATTTGAGTTTCC 600

Qy 601 ATTGCTTAAATTTCAAAATATGGAATTAACAATGTGTTTATCATATTCAGAAAAATGGA 660
    |||
Db 601 ATTGCTTAAATTTCAAAATATGGAATTAACAATGTGTTTATCATATTCAGAAAAATGGA 660

Qy 661 CGTAGCTTTCATCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAAATGCA 720
    |||
Db 661 CGTAGCTTTCATCTCACAGGACTCTGACTGTAAGAGTAGTAGGCTCTCCAAAAATGCA 720

Qy 721 GTGCCCCCTGTGATCCATTCACTTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780
    |||
Db 721 GTGCCCCCTGTGATCCATTCACTTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780

Qy 781 GAGCTACTCAATCCCTGTAGGCTCTATTTAGTATTTCTGATGGATTCTCGCAATGAGTT 840
    |||
Db 781 GAGCTACTCAATCCCTGTAGGCTCTATTTAGTATTTCTGATGGATTCTCGCAATGAGTT 840

Qy 841 TGTGGACCAATTTGATGAAAAAACCCTGATGACATCACTATTGATGTCACCAATTAACGAA 900
    |||
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[illegible]

Search completed: December 14, 2005, 15:29:31  
Job time : 1711 secs

November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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Db	901	AGTATAAGTCATAGTAGAACAGAAGATGAACAAGAACTCAGATTTTGGAGCATCAAGAAA	960
Qy	961	GTTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCTCATGCTAGAGTGCCAAAGGGCAA	1020
Db	961	GTTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCTCATGCTAGAGTGCCAAAGGGCAA	1020
Qy	1021	GTTTGCCAAAGCAGCCCAAGGTGAACGAGAAAGTGCCAGCTCCAAAGATACACAGTGGAACTG	1080
Db	1021	GTTTGCCAAAGCAGCCCAAGGTGAACGAGAAAGTGCCAGCTCCAAAGATACACAGTGGAAAAA	1080
Qy	1081	GCTTGTGGTTTGGAGCCACAGTCTCTGCTAGTG	1113
Db	1081	TGCAAGGAACGTGAAGAAAAAATAATTTTATGTG	1113

## RESULT. T 3

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US-11-144-987-13
; Sequence 13, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-13

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Query Match	52.0%;	Score 1073;	DB 7;	Length 2709;
Best Local Similarity	97.8%;	Pred. No. 0;		
Matches 1088;	Conservative 0;	Mismatches 25;	Indels 0;	Gaps 0;
QY	1	ATCACACTCTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC	60	
DB	1	ATGGTGGTCTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC	60	
QY	61	TCAGAACGCTGCGATGACTCGGGACTAGACACCATGAGCGCAATTCCAAGTGTTTGAAGAT	120	
DB	61	TCAGAACGCTGCGATGACTCGGGACTAGACACCATGAGCGCAATTCCAAGTGTTTGAAGAT	120	
QY	121	GAGCCAGCTCGCATCAAGTGCCTCCACTCTTTGGAACACTTCTTGAATTCCTCAACTACAGCAC	180	
DB	121	GAGCCAGCTCGCATCAAGTGCCTCCACTCTTTGGAACACTTCTTGAATTCCTCAACTACAGCAC	180	
QY	181	GCCCATTCAGCTGGCCTTACTCTGATCTGTGTATTGGACTAGGCAGGACCGGGACCTTGAG	240	
DB	181	GCCCATTCAGCTGGCCTTACTCTGATCTGTGTATTGGACTAGGCAGGACCGGGACCTTGAG	240	
QY	241	GAGCCCAATTAACTTTCGCGCTTCCCGGAAACCGCATTAGTAAGGAGAAAGATGTGCTGTGG	300	
DB	241	GAGCCCAATTAACTTTCGCGCTTCCCGGAAACCGCATTAGTAAGGAGAAAGATGTGCTGTGG	300	
QY	301	TTCCGGGCCACTCTCTCAATGACACTGGGCAACTATACCTGCACTGTTAAGGAACACTACA	360	
DB	301	TTCCGGGCCACTCTCTCAA TGA CACTGGCAACTATACCTGCACTGTTAAGGAACACTACA	360	
QY	361	TATTGCAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC	420	
DB	361	TATTGCAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC	420	
QY	421	CCCATGAAACTCCCAAGTGCAATAAAGTGTATATAGAAATTCAGGAGATCACTTGT	480	

421	DB	CCCATGAAACTCCAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT	480
481	QY	CCAAATGTAGATGGATATTTTCCCTCCAGTGTCAAACCGCATATCACTTGGTATATGGGC	540
481	DB	CCAAATGTAGATGGATATTTTCCCTCCAGTGTCAAACCGCATATCACTTGGTATATGGGC	540
541	QY	TGTTATAAAATACAGAATTTTAAATATATGTAAATACCCGAGGTATGAACTTGAGTTTCCTC	600
541	DB	TGTTATAAAATACAGAATTTTAAATATATGTAAATACCCGAGGTATGAACTTGAGTTTCCTC	600
601	QY	ATTGCCCTTAATTTCAAATAATGGAATTCACATGTGTTGTTACATATCCAGAAAAATGGA	660
601	DB	ATTGCCCTTAATTTCAAATAATGGAATTCACATGTGTTGTTACATATCCAGAAAAATGGA	660
661	QY	CGTACGTTTCATCTCCACAGGACTCTGACGTGTAAGGTAGTAGGCTCTCCAAAAATGCA	720
661	DB	CGTACGTTTCATCTCCACAGGACTCTGACGTGTAAGGTAGTAGGCTCTCCAAAAATGCA	720
721	QY	GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTATCAGAAAGAACACAGAGAG	780
721	DB	GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTATCAGAAAGAACACAGAGAG	780
781	QY	GAGCTACTCATCTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTTCTGCAATAGGTT	840
781	DB	GAGCTACTCATCTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTTCTGCAATAGGTT	840
841	QY	TGTTGGNCACTTGAATGGAAAAAACTGTGATGACATCACTATTGATGTCACCATTAACGAA	900
841	DB	TGTTGGNCACTTGAATGGAAAAAACTGTGATGACATCACTATTGATGTCACCATTAACGAA	900
901	QY	AGTATAAGTCAATAGTAGAAACAGAAGATGAAACAAAGAACTCAGATTTTGAAGCATCAAGAAA	960
901	DB	AGTATAAGTCAATAGTAGAAACAGAAGATGAAACAAAGAACTCAGATTTTGAAGCATCAAGAAA	960
961	QY	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGTCGTCTAGTAAAGTGCCAAAGCGCAA	1020
961	DB	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGTCGTCTAGTAAAGTGCCAAAGCGCAA	1020
1021	QY	GTTTGCCAAAGCACCAGGTGAAGCAGAAAGTSCCAGCTCCAAAGATACACAGTGGAACTG	1080
1021	DB	GTTTGCCAAAGCACCAGGTGAAGCAGAAAGTSCCAGCTCCAAAGATACACAGTGGAACTG	1080
1081	QY	GCTTGTGGTTTTGGAGCCACAGTCTGCTAGTG	1113
1081	DB	TGCAAGCAACCTGAAGAAAAATAAATTTTAGTG	1113

## RESULT 4

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RES001 4
US-11-144-987-21
; Sequence 21, Application US/11144987
; Publication No. US2005027265A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Vancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-21

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Query Match 51.8%; Score 1069.6; DB 7; Length 2748;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



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Db 661 CGTAGGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTACCTAAATGATCATGTGTCTATGAGAAAGAACAGGAGAG 780
Db 721 GTGCCCCCTGTGATCCATTACCTAAATGATCATGTGTCTATGAGAAAGAACAGGAGAG 780
Qy 781 GAGCTACTCATTCCTCTGACGGTCTATTTAGTTTCTGATGGAATTCCTGCAATGAGGTT 840
Db 781 GAGCTACTCATTCCTCTGACGGTCTATTTAGTTTCTGATGGAATTCCTGCAATGAGGTT 840
Qy 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTAATGATGTCACCATTTAAGCAA 900
Db 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTAATGATGTCACCATTTAAGCAA 900
Qy 901 AGTATAAGTCATAGTAGAAGCAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAAGCAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAGGTTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGCA 1076
Db 1021 GTTGCCAAAGCAGCAGGTTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGCA 1076
```

## RESULT 6

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US-11-144-987-25
; Sequence 25, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-25
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Query Match 51.8%; Score 1069.6; DB 7; Length 2754;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 ATGACACTTCTGTGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC 60
Db 1 ATGAGTCTTCTGTGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC 60
Qy 61 TCAGAACGCTGCGATGATCGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTAAGAT 120
Db 61 TCAGAACGCTGCGATGATCGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTAAGAT 120
Qy 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAATTTCAACTACAGGACA 180
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAATTTCAACTACAGGACA 180
Qy 181 GCCCATTTACCTGGCCCTTACTCTGATCTGTATTTGGACTAGGAGGACCGGGACCTTGAG 240
Db 181 GCCCATTTACCTGGCCCTTACTCTGATCTGTATTTGGACTAGGAGGACCGGGACCTTGAG 240
Qy 241 GAGCCCAATTAACTTCGCGCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCCAATTAACTTCGCGCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 300
```

```
Db 241 GAGCCCAATTAACTTCGCGCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 300
Qy 301 TTCCGGCCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTTAAAGAACACTACA 360
Db 301 TTCCGGCCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTTAAAGAACACTACA 360
Qy 361 TATTGACAGCAAAAGTTGCAATTTCCCTTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACAGCAAAAGTTGCAATTTCCCTTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 421 CCATGAAACTCCCATGTCATAAACTGTATATATAAGAAATGCGCATTTGAGAGATCACTGT 480
Db 421 CCATGAAACTCCCATGTCATAAACTGTATATATAAGAAATGCGCATTTGAGAGATCACTGT 480
Qy 481 CCAAAATGTAGATGGAATTTTCCCTCCAGTGTCAAAACCGACTATACCTTGGTATATAGGGC 540
Db 481 CCAAAATGTAGATGGAATTTTCCCTCCAGTGTCAAAACCGACTATACCTTGGTATATAGGGC 540
Qy 541 TGTATAAAATACAGAAATTTTAAATAATGTAATAACCGAAGGTATGAACCTTTGAGTTTCCCTC 600
Db 541 TGTATAAAATACAGAAATTTTAAATAATGTAATAACCGAAGGTATGAACCTTTGAGTTTCCCTC 600
Qy 601 ATTGCTCTTAATTTCAAAATTAATGGAATTAACATGTGTTGTTACATATCCAGAAAAATGGA 660
Db 601 ATTGCTCTTAATTTCAAAATTAATGGAATTAACATGTGTTGTTACATATCCAGAAAAATGGA 660
Qy 661 CGTACGTTTCACTCTCACCGAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Db 661 CGTACGTTTCACTCTCACCGAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTACCTAAATGATCATGTGTCTATGAGAAAGAACAGGAGAG 780
Db 721 GTGCCCCCTGTGATCCATTACCTAAATGATCATGTGTCTATGAGAAAGAACAGGAGAG 780
Qy 781 GAGCTACTCATTCCTCTGATCGGTCATTTTAGTTTCTGATGGAATTCCTGCAATGAGGTT 840
Db 781 GAGCTACTCATTCCTCTGATCGGTCATTTTAGTTTCTGATGGAATTCCTGCAATGAGGTT 840
Qy 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTATTTGATGTCACCATTTAAGCAA 900
Db 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTATTTGATGTCACCATTTAAGCAA 900
Qy 901 AGTATAAGTCATAGTAGAAGCAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAAGCAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAGGTTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGA 1076
Db 1021 GTTGCCAAAGCAGCAGGTTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGA 1076
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## RESULT 7

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US-11-144-987-1
; Sequence 1, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
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; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-1

Query Match      51.8%; Score 1069.2; DB 7; Length 2733;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGACACTCTGTGGTGTGTAGTGTCTCTACTTTTATGGAACTCTGCAAAAGTATGCC 60
   |||
Db 1 ATGGCTCTCTGTGGTGTGTAGTGTCTCTACTTTTATGGAACTCTGCAAAAGTATGCC 60

QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 120
   |||
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 120

QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTTGAACACTCTTGAACACTTGAACACTACACACA 180
   |||
Db 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTGAACACTTGAACACTACACACA 180

QY 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTATTTGGACTAGGACGAGCCGGACCTTGAG 240
   |||
Db 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTATTTGGACTAGGACGAGCCGGACCTTGAG 240

QY 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300
   |||
Db 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300

QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAAGAACACTACA 360
   |||
Db 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAAGAACACTACA 360

QY 361 TATTGACAGAAAGTTCATTTCCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTC 420
   |||
Db 361 TATTGACAGAAAGTTCATTTCCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTC 420

QY 421 CCCATGAAACTCCCAGTGCATAAATCTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
   |||
Db 421 CCCATGAAACTCCCAGTGCATAAATCTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480

QY 481 CCAATGTATAGTGGATATTTTCTCCAGTGTCAAAACCGCATATCACTTTGGTATATGGGC 540
   |||
Db 481 CCAATGTATAGTGGATATTTTCTCCAGTGTCAAAACCGCATATCACTTTGGTATATGGGC 540

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAACCTTGAGTTTCC 600
   |||
Db 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAACCTTGAGTTTCC 600

QY 601 ATTGCCTTAATTTCAAATTAATGAAATTAACATGTGTTGTTTACATATCCAGAAATGGA 660
   |||
Db 601 ATTGCCTTAATTTCAAATTAATGAAATTAACATGTGTTGTTTACATATCCAGAAATGGA 660

QY 661 CGTAGCTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCAAAAATGCA 720
   |||
Db 661 CGTAGCTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCAAAAATGCA 720

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
   |||
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTTCTGATGGAATTCGCAATGAGGTT 840
   |||
Db 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTTCTGATGGAATTCGCAATGAGGTT 840

QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
   |||
Db 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 900

QY 901 AGTATAAGTCATAGTAGAAGATGAAACCAAGAACTCAGATTTTGTAGCATCAAGAAA 960
   |||
Db 901 AGTATAAGTCATAGTAGAAGATGAAACCAAGAACTCAGATTTTGTAGCATCAAGAAA 960
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QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTCATGTAGAGTGCCAAAGCGCAA 1020
   |||
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTCATGTAGAGTGCCAAAGCGCAA 1020

QY 1021 GTTGCCAAAGCAGCCCAAGGTGAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074
   |||
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074

RESULT 8
US-11-144-987-3
; Sequence 3, Application US/11144987
; Publication No. US2005027265S1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Dise
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-3

Query Match      49.3%; Score 1017; DB 7; Length 2703;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 120
   |||
Db 997 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGGAAGAT 1056

QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTGAACACTTCAACTACACACA 180
   |||
Db 1057 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTGAACACTTCAACTACACACA 1116

QY 181 GCCCATTTCAGCTGGGCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 240
   |||
Db 1117 GCCCATTTCAGCTGGGCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 1176

QY 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300
   |||
Db 1177 GAGCCAAATTAACCTCCGCTCCCGAGAACCCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 1236

QY 301 TTCCGGCCCACTCTCTCAATGACACTGCGCACTATCTGCACTGTTAGGAAACACTACA 360
   |||
Db 1237 TTCCGGCCCACTCTCTCAATGACACTGCGCACTATCTGCACTGTTAGGAAACACTACA 1296

QY 361 TATTGCAGCAAAAGTTGCAATTTCCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTC 420
   |||
Db 1297 TATTGCAGCAAAAGTTGCAATTTCCCTTGGAAAGTGTTCAAAAGACAGCTGTTTCAATTC 1356

QY 421 CCCATGAAATCCCAAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
   |||
Db 1357 CCCATGAAATCCCAAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 1416

QY 481 CCAATGTAGATGGATATTTTCTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 540
   |||
Db 1417 CCAATGTAGATGGATATTTTCTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 1476

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGGATGTAAGACTTTGATTTCC 600
   |||
Db 1477 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGGATGTAAGACTTTGATTTCC 1536

QY 601 ATTGCCTTAATTTCAAATAATGGAATTAACATGTGTTGTACATATCCAGAAATGGA 660
```

```
Db 1537 ATTGCCCTTAATTTCAATAATGGAATTTACACATGTGTTGTTACATATCCAGAAAATGGA 1596
Qy 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGTAGTAGGCTCTCAAAAAATGCA 720
Db 1597 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGTAGTAGGCTCTCAAAAAATGCA 1656
Qy 721 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
Db 1657 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 1716
Qy 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTTT 840
Db 1717 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTTT 1776
Qy 841 TGGTGGACCAATGATGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
Db 1777 TGGTGGACCAATGATGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 1836
Qy 901 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960
Db 1837 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1896
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTGCACAAAGCGGAA 1020
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTGCACAAAGCGGAA 1956
Qy 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGGAA 1077
Db 1957 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGGAA 2013

RESULT 9
US-11-144-987-5
; Sequence 5, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-5

Query Match 49.3%; Score 1017; DB 7; Length 2709;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCACTAGAGCAAAATCCAAAGTGTGTTGAAGAT 120
Db 997 TCAGAACGCTGCGATGACTGGGACTAGACACCACTAGAGCAAAATCCAAAGTGTGTTGAAGAT 1056

Qy 121 GAGCCAGCTGCGATCAAGTGCCCACTCTTTGAACACTCTTTGAAATTCACATCAGACACA 180
Db 1057 GAGCCAGCTGCGATCAAGTGCCCACTCTTTGAACACTCTTTGAAATTCACATCAGACACA 1116

Qy 181 GCCATTTCAGTGGCTTACTCTGATCTGTTGATGAGTGGAGTGGAGGACCGGACCTTGAG 240
Db 1117 GCCATTTCAGTGGCTTACTCTGATCTGTTGATGAGTGGAGTGGAGGACCGGACCTTGAG 1176

Qy 241 GAGCCAAATTAATTTCCGCCCTCCCGAGAACCGCATTAAGTAGGAGAAAGATGTGCTGTGG 300
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RESULT 10
US-11-144-987-7
; Sequence 7, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
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Db 1177 GAGCCAAATTAATTTCCGCCCTCCCGAGAACCGCATTAAGTAGGAGAAAGATGTGCTGTGG 1236
Qy 301 TTCCGCCCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTTAAGGAACACTACA 360
Db 1237 TTCCGCCCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTTAAGGAACACTACA 1296
Qy 361 TATTGACGAGCAAAAGTTGCAATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 1297 TATTGACGAGCAAAAGTTGCAATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 1356
Qy 421 CCCATGAAACTCTCCAGTGCATAAATCTGTATATAGAATAAGGCATTTAGAGATCACTTGT 480
Db 1357 CCCATGAAACTCTCCAGTGCATAAATCTGTATATAGAATAAGGCATTTAGAGATCACTTGT 1416
Qy 481 CCAAAATGATAGTATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db 1417 CCAAAATGATAGTATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 1476
Qy 541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAAAGGTATGAATTTGAGTTTCCCTC 600
Db 1477 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAAAGGTATGAATTTGAGTTTCCCTC 1536
Qy 601 ATTCCTTTAATTTCAAAATTAAGCAATGTTGTTTACATATCCAGAAAAATGGA 660
Db 1537 ATTCCTTTAATTTCAAAATTAAGCAATGTTGTTTACATATCCAGAAAAATGGA 1596
Qy 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGTAGTAGGCTCTCAAAAAATGCA 720
Db 1597 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGTAGTAGGCTCTCAAAAAATGCA 1656
Qy 721 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
Db 1657 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 1716
Qy 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTTT 840
Db 1717 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTTT 1776
Qy 841 TGGTGGACCAATGATGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
Db 1777 TGGTGGACCAATGATGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 1836
Qy 901 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960
Db 1837 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1896
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTGCACAAAGCGGAA 1020
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTGCACAAAGCGGAA 1956
Qy 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGGAA 1077
Db 1957 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGGAA 2013
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; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-144-987-7

Query Match 49.3%; Score 1017; DB 7; Length 2709;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGCAAAATCCAAGTGTGTTGAAGAT 120

Db 997 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGAAATCCAAGTGTGTTGAAGAT 1056

QY 121 GAGCCAGCTCGCATCAAGTGCACACTCTTTGAACTCTTTGAAATTCAACTACAGACA 180

Db 1057 GAGCCAGCTCGCATCAAGTGCACACTCTTTGAACTCTTTGAAATTCAACTACAGACA 1116

QY 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGAGGACCGGACCTTGAG 240

Db 1117 GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGAGGACCGGACCTTGAG 1176

QY 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 300

Db 1177 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 1236

QY 301 TTCGGCCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAAGGAACACTACA 360

Db 1237 TTCGGCCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAAGGAACACTACA 1296

QY 361 TATTGAGCAAAAGTTCATTTCCCTTGGAAAGTGTTCAAAAAGACAGCTGTTTCAATTCC 420

Db 1297 TATTGAGCAAAAGTTCATTTCCCTTGGAAAGTGTTCAAAAAGACAGCTGTTTCAATTCC 1356

QY 421 CCCATGAATCTCCAGTCGATAAATCTGTATATAGAAATGAGCAATGAGGATCACTTGT 480

Db 1357 CCCATGAATCTCCAGTCGATAAATCTGTATATAGAAATGAGCAATGAGGATCACTTGT 1416

QY 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540

Db 1417 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 1476

QY 541 TGTATAAATACAGAAATTTTAATGTAATGTAATACCGAAGGTATGAACTTGATTTCTTC 600

Db 1477 TGTATAAATACAGAAATTTTAATGTAATGTAATACCGAAGGTATGAACTTGATTTCTTC 1536

QY 601 ATTGCCTTAATTTCAAATTAATGAAATTAACAATGTTGTTTACATATCCAGAAATGGA 660

Db 1537 ATTGCCTTAATTTCAAATTAATGAAATTAACAATGTTGTTTACATATCCAGAAATGGA 1596

QY 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCAAAAAATGCA 720

Db 1597 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCAAAAAATGCA 1656

QY 721 GTGCCCCCTGTGATCCATTCACTTAATGATCATGTGTTCTATGAGAAAGAACCCAGAGAG 780

Db 1657 GTGCCCCCTGTGATCCATTCACTTAATGATCATGTGTTCTATGAGAAAGAACCCAGAGAG 1716

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGGATTTCTCGCAATGAGTT 840

Db 1717 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGGATTTCTCGCAATGAGTT 1776

QY 841 TGGTGGACCATTTGATGGAAAAAACCTGTATGATCATCACTATTGATGTCTCAATTAACGAA 900

Db 1777 TGGTGGACCATTTGATGGAAAAAACCTGTATGATCATCACTATTGATGTCAATTAACGAA 1836

QY 901 AGTATAAGTCATAGTAGACAGAGATGAAACAAGNACTCAGATCTCAGATTTTGAGCATCAAGAAA 960

Db 1837 AGTATAAGTCATAGTAGACAGAGATGAAACAAGNACTCAGATCTCAGATTTTGAGCATCAAGAAA 1896

QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCAATGCTAGAAAGTGCACCAAGCGGAA 1020

Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCAATGCTAGAAAGTGCACCAAGCGGAA 1956

QY 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAA 1077

Db 1957 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAA 2013

RESULT 11

US-11-144-987-15

; Sequence 15, Application US/11144987

; Publication No. US20050272655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; FILE REFERENCE: REG 2050A

; CURRENT APPLICATION NUMBER: US/11/144,987

; CURRENT FILING DATE: 2005-06-03

; PRIOR APPLICATION NUMBER: 60/577,023

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 2748

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-144-987-15

Query Match 49.2%; Score 1015; DB 7; Length 2748;

Best Local Similarity 100.0%; Pred. No. 4.7e-315;

Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CTCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCCAAGTGTGTTGAAGA 119

Db 1044 CTCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCCAAGTGTGTTGAAGA 1103

QY 120 TGAGCCAGCTCGCATCAAGTGCCTCTTTGAACTCTTTGAACTCTTTGAAATTCAACTACAGCAC 179

Db 1104 TGAGCCAGCTCGCATCAAGTGCCTCTTTGAACTCTTTGAACTCTTTGAAATTCAACTACAGCAC 1163

QY 180 AGCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGACCGGACCTTGA 239

Db 1164 AGCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGACCGGACCTTGA 1223

QY 240 GGAGCCAAATTAACCTTCGCTCCGCTCCCGAGAACCGCATTAAGTAAGGAGAAAGATGTGCTGTG 299

Db 1224 GGAGCCAAATTAACCTTCGCTCCGCTCCCGAGAACCGCATTAAGTAAGGAGAAAGATGTGCTGTG 1283

QY 300 GTTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCTGATGTTAAGGAACACTAC 359

Db 1284 GTTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCTGATGTTAAGGAACACTAC 1343

QY 360 ATATTGGACGAAAGTTGCAATTTCCCTTCGAAAGTGTTCAAAAGACAGCTGTTCAATTC 419

Db 1344 ATATTGGACGAAAGTTGCAATTTCCCTTCGAAAGTGTTCAAAAGACAGCTGTTCAATTC 1403

QY 420 CCCCATGAAACTCCAGTGCATAAACTGTATAGAAATATGCAATTCAGAGGATCACTTG 479

Db 1404 CCCCATGAAACTCCAGTGCATAAACTGTATAGAAATATGCAATTCAGAGGATCACTTG 1463

QY 480 TCCAAATGTAGATGATATTTTCCCTTCAGTGTCAAACCGACTATCACTTGGTATATGGG 539

Db 1464 TCCAAATGTAGATGATATTTTCCCTTCAGTGTCAAACCGACTATCACTTGGTATATGGG 1523

QY 540 CTGTTTATAAATACAGAAATTTTAATGTAATACCCGAAAGTATGAATTCAGTTTCT 599

Db 1524 CTGTTTATAAATACAGAAATTTTAATGTAATACCCGAAAGTATGAATTCAGTTTCT 1583

QY 600 CATTCGCTTTAATTTCAAATAATGGAATTAACACATGTGTGTTACATATCCAGAAATCG 659

Db 1584 CATTCGCTTTAATTTCAAATAATGGAATTAACACATGTGTGTTACATATCCAGAAATCG 1643

QY 660 ACGTACGTTTCAATCTCAACGAGACTCTGCTGTAAGGTAGTAGGCTCTCCAAAAAATGC 719



Db 1644 ACCTACGTTTCTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATGC 1703  
Qy 720 AGTCCCGCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATCAGAAAGAACCCAGGAGA 779  
Db 1704 AGTGCCCGCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATCAGAAAGAACCCAGGAGA 1763  
Qy 780 GGAGCTACTCATTCCTCTGACGGTCTATTTTGTAGTTTCTGATGGATTCTCGCAATGAGGT 839  
Db 1764 GGAGCTACTCATTCCTCTGACGGTCTATTTTGTAGTTTCTGATGGATTCTCGCAATGAGGT 1823  
Qy 840 TTGGTGACCAATGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGA 899  
Db 1824 TTGGTGACCAATGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGA 1883  
Qy 900 AAGTATAAGTCATAGTAGACAGAGATGAACAGAACTCAGATTTTTGAGCATCAAGAA 959  
Db 1884 AAGTATAAGTCATAGTAGACAGAGATGAACAGAACTCAGATTTTTGAGCATCAAGAA 1943  
Qy 960 AGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGCTAGAGTGCCTCAAGGCGGA 1019  
Db 1944 AGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGCTAGAGTGCCTCAAGGCGGA 2003  
Qy 1020 AGTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTG 1074  
Db 2004 AGTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTG 2058

## RESULT 12

US-11-144-987-17

; Sequence 17, Application US/11144987

; Publication No. US20050272655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; CURRENT APPLICATION NUMBER: US/11/144,987

; CURRENT FILING DATE: 2005-06-03

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 2754

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-144-987-17

## Query Match

Best Local Similarity 100.0%; Pred. No. 4.7e-315;

Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 CTCAGAACGCTGGATGACCTGGGACCTAGACACCATGAGGCAAAATCCAAAGTGTTCGAAGA 119  
Db 1044 CTCAGAACGCTGGATGACCTGGGACCTAGACACCATGAGGCAAAATCCAAAGTGTTCGAAGA 1103  
Qy 120 TGAGCCAGCTCGCATCAAGTGCCCACTCTTTTGAACACTCTTGAATTCAACTACAGCAC 179  
Db 1104 TGAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTTGAATTCAACTACAGCAC 1163  
Qy 180 AGCCATTCAGCTGGCCCTTACTCTGATCTGGTATTTGAGCTAGGAGGACCGGACCTTGA 239  
Db 1164 AGCCATTCAGCTGGCCCTTACTCTGATCTGGTATTTGAGCTAGGAGGACCGGACCTTGA 1223  
Qy 240 GGAGCCAAATTAACCTCCGCTCCCGAGAACCCATTAGTAAGGAGAAATGCTGCTG 299  
Db 1224 GGAGCCAAATTAACCTCCGCTCCCGAGAACCCATTAGTAAGGAGAAATGCTGCTG 1283  
Qy 300 GTTCCCGCCCACTCTCCTCAATGACACTGGAACATATACCTGCTGTAAGGAAACACTAC 359

Db 1284 GTTCCCGCCCACTCTCCTCAATGACACTGGAACATATACCTGCTGATGTTAAGGAACACTAC 1343  
Qy 360 ATATTGCAGCAAAAGTTGCATTTCCCTTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTTC 419  
Db 1344 ATATTGCAGCAAAAGTTGCATTTCCCTTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTTC 1403  
Qy 420 CCCCATGAAACTCCCAGTGCATAAACTGTATATAGAATATATAGGAATATGGCAATTCAGAGGATCACTTG 479  
Db 1404 CCCCATGAAACTCCCAGTGCATAAACTGTATATAGAATATATGGCAATTCAGAGGATCACTTG 1463  
Qy 480 TCCAAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGACTATATCACTGGTATATATGGG 539  
Db 1464 TCCAAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGACTATATCACTGGTATATATGGG 1523  
Qy 540 CTGTTATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAATTTAGTTTTCCT 599  
Db 1524 CTGTTATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAATTTAGTTTTCCT 1583  
Qy 600 CATTTGCTTAAATTTCAAAATTAATGAAATTAACACATGTGTTTGTACATATCCAGAAAAATGG 659  
Db 1584 CATTTGCTTAAATTTCAAAATTAATGAAATTAACACATGTGTTTGTACATATCCAGAAAAATGG 1643  
Qy 660 ACCTAGCTTTTCACTCTCAACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGC 719  
Db 1644 ACCTAGCTTTTCACTCTCAACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGC 1703  
Qy 720 AGTGCCCGCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATCAGAAAGAACCCAGGAGA 779  
Db 1704 AGTGCCCGCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATCAGAAAGAACCCAGGAGA 1763  
Qy 780 GGAGCTACTCATTCCTCTGACGGTCTATTTTGTAGTTTCTGATGGATTCTCGCAATGAGGT 839  
Db 1764 GGAGCTACTCATTCCTCTGACGGTCTATTTTGTAGTTTCTGATGGATTCTCGCAATGAGGT 1823  
Qy 840 TTGGTGACCAATGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGA 899  
Db 1824 TTGGTGACCAATGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATTAACGA 1883  
Qy 900 AAGTATAAGTCATAGTAGACAGAGATGAACAGAACTCAGATTTTTGAGCATCAAGAA 959  
Db 1884 AAGTATAAGTCATAGTAGACAGAGATGAACAGAACTCAGATTTTTGAGCATCAAGAA 1943  
Qy 960 AGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGCTAGAGTGCCTCAAGGCGGA 1019  
Db 1944 AGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGCTAGAGTGCCTCAAGGCGGA 2003  
Qy 1020 AGTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTG 1074  
Db 2004 AGTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTG 2058

## RESULT 13

US-11-144-987-19

; Sequence 19, Application US/11144987

; Publication No. US20050272655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; FILE REFERENCE: REG 2090A

; CURRENT APPLICATION NUMBER: US/11/144,987

; CURRENT FILING DATE: 2005-06-03

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 19

; LENGTH: 2754

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-144-987-19

Query Match		49.2%;	Score 1015;	DB 7;	Length 2754;
Best Local Similarity		100.0%;	Pred. No. 4.7e-315;		
Matches 1015;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	60	CTCAGAACCTCGATGATCTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGA	119		
DB	1044	CTCAGAACCTCGATGATCTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGA	1103		
QY	120	TGAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACATCTCTTGAATAATCAACTACAGCAC	179		
DB	1104	TGAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACATCTCTTGAATAATCAACTACAGCAC	1163		
QY	180	AGCCCATTCAGCTGGCCTTACTCTGATCTGTGATTGGACTAGGCAGGACCGGACCTTGA	239		
DB	1164	AGCCCATTCAGCTGGCCTTACTCTGATCTGTGATTGGACTAGGCAGGACCGGACCTTGA	1223		
QY	240	GGAGCCAATTAACTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTG	299		
DB	1224	GGAGCCAATTAACTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTG	1283		
QY	300	GTTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAAGAACACTAC	359		
DB	1284	GTTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAAGAACACTAC	1343		
QY	360	ATATTGCAGCAAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTCAATTTC	419		
DB	1344	ATATTGCAGCAAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTCAATTTC	1403		
QY	420	CCCATGAAACTCCAGTGCAATAACTGTATATAGAAATGATGCAATTCAGAGGATCACTTG	479		
DB	1404	CCCATGAAACTCCAGTGCAATAACTGTATATAGAAATGATGCAATTCAGAGGATCACTTG	1463		
QY	480	TCCAATGTAGATGATATTTTCCTTCAGTCTCAACCGCACTATCACTTGTGTATATGG	539		
DB	1464	TCCAATGTAGATGATATTTTCCTTCAGTCTCAACCGCACTATCACTTGTGTATATGG	1523		
QY	540	CTGTTATAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTCAGTTTCT	599		
DB	1524	CTGTTATAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTCAGTTTCT	1583		
QY	600	CATTGCTTAATTCAAATAATGGAATTPACATGTGTGTGTTACATATCCAGAAATGG	659		
DB	1584	CATTGCTTAATTCAAATAATGGAATTPACATGTGTGTGTTACATATCCAGAAATGG	1643		
QY	660	AGTAGCTTTTCATCTCACGAGACTCTGACTCTAAAGGTAGTAGGCTCTCCAAAAATGC	719		
DB	1644	AGTAGCTTTTCATCTCACGAGACTCTGACTCTAAAGGTAGTAGGCTCTCCAAAAATGC	1703		
QY	720	AGTGCCCTCTGTATCCATTCACCTAATGATCATGTGTTCTATGAGAAAGAACCCAGGAGA	779		
DB	1704	AGTGCCCTCTGTATCCATTCACCTAATGATCATGTGTTCTATGAGAAAGAACCCAGGAGA	1763		
QY	780	GGAGTACTCATCTCGTACGGTCTATTTTATGTTTCTGATGGATTTCTCGCAATGAGGT	839		
DB	1764	GGAGTACTCATCTCGTACGGTCTATTTTATGTTTCTGATGGATTTCTCGCAATGAGGT	1823		
QY	840	TTGTGGACCATTTGAGAAAAAACCTGATCACATCACTATTGATGTCACCATTAACGA	899		
DB	1824	TTGTGGACCATTTGAGAAAAAACCTGATCACATCACTATTGATGTCACCATTAACGA	1883		
QY	900	AAATATAAGTCATAGTAGAACAGAGATGAAACAAAGAACTCAGATTTTGGAGCATCAAGAA	959		
DB	1884	AAATATAAGTCATAGTAGAACAGAGATGAAACAAAGAACTCAGATTTTGGAGCATCAAGAA	1943		
QY	960	AGTTACCTCTGAGGATCTCAAGCGGAGCTATCTGTCTCATGTAGAAAGTGC AAAAGCGCA	1019		
DB	1944	AGTTACCTCTGAGGATCTCAAGCGGAGCTATCTGTCTCATGTAGAAAGTGC AAAAGCGCA	2003		
QY	1020	AGTTGCCAAGCAGCCAGGTGAACGAGAAAGTGCAGCTCCAGATACACAGTG	1074		
DB	2004	AGTTGCCAAGCAGCCAGGTGAACGAGAAAGTGCAGCTCCAGATACACAGTG	2058		

RESULT 14		US-10-750-185-48357/c	
		; Sequence 48357, Application US/10750185	
		; Publication No. US20050260603A1	
		; GENERAL INFORMATION:	
		; APPLICANT: MMI GENOMICS, INC.	
		; APPLICANT: DENISE, Sue K.	
		; APPLICANT: KERR, Richard	
		; APPLICANT: ROSENFELD, David	
		; APPLICANT: HOLM, Tom	
		; APPLICANT: BATES, Stephen	
		; APPLICANT: FANTIN, Dennis	
		; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS	
		; FILE REFERENCE: MM1100-2	
		; CURRENT APPLICATION NUMBER: US/10/750,185	
		; CURRENT FILING DATE: 2003-12-31	
		; PRIOR APPLICATION NUMBER: US 60/437,482	
		; PRIOR FILING DATE: 2002-12-31	
		; NUMBER OF SEQ ID NOS: 64922	
		; SOFTWARE: PatentIN version 3.1	
		; SEQ ID NO 48357	
		; LENGTH: 5178	
		; TYPE: DNA	
		; ORGANISM: Bovine 19866881094067	
		US-10-750-185-48357	
Query Match		5.5%;	Score 114.2; DB 6; Length 5178;
Best Local Similarity		84.8%;	Pred. No. 1.6e-25;
Matches 128;		Conservative 0;	Mismatches 23; Indels 0; Gaps 0;
QY	901	AGTATAAGTCATAGTAGAACACAGAACTGAAACAAAGAACTCAGATTTTGAGCATCAAGAAA	960
DB	1423	AGTATAAGTCATAGTAGAACACAGAACTGAAACAAAGAACTCAGATTTTGAGCATCAAGAAA	1364
QY	961	GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTGC AAAAGCGGAA	1020
DB	1363	GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTGC AAAAGCGGAG	1304
QY	1021	GTTGCCAAGCAGCCCAAGGTGAAGCAGAAAG	1051
DB	1303	GTTGCCAAGCAGCCCAAGGTGAAGCAGAAAG	1273
RESULT 15		US-10-750-185-48351/c	
		; Sequence 48351, Application US/10750185	
		; Publication No. US20050260603A1	
		; GENERAL INFORMATION:	
		; APPLICANT: MMI GENOMICS, INC.	
		; APPLICANT: DENISE, Sue K.	
		; APPLICANT: KERR, Richard	
		; APPLICANT: ROSENFELD, David	
		; APPLICANT: HOLM, Tom	
		; APPLICANT: BATES, Stephen	
		; APPLICANT: FANTIN, Dennis	
		; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS	
		; FILE REFERENCE: MM1100-2	
		; CURRENT APPLICATION NUMBER: US/10/750,185	
		; CURRENT FILING DATE: 2003-12-31	
		; PRIOR APPLICATION NUMBER: US 60/437,482	
		; PRIOR FILING DATE: 2002-12-31	
		; NUMBER OF SEQ ID NOS: 64922	
		; SOFTWARE: PatentIN version 3.1	
		; SEQ ID NO 48351	
		; LENGTH: 1388	
		; TYPE: DNA	
		; ORGANISM: Bovine 19866880606021	
		US-10-750-185-48351	
Query Match		2.9%;	Score 60.2; DB 6; Length 1388;
Best Local Similarity		78.0%;	Pred. No. 1.4e-08;
Matches 85;		Conservative 0;	Mismatches 23; Indels 1; Gaps 1;



Qy	274	ATTAGTAAGGAGAAAGATGTGCTGTGTTCCGGCCCACTCTC-CTCAATGACACTGGCAA	332
Db	1388	ATTAGTAAGGAGAAAGACGTGCTCTGTTCCGGCCCACTCTTCTCAATGACACGGGAAA	1329
Qy	333	CTATACCTGCATGTTAAGGAACACTACATATTGCAGCAAGTTGCATTT	381
Db	1328	CTATACCTGCATGTTAAGGTAGGCTGACGCTTGTGTGTTTCCCTTT	1280

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Job time : 264 secs

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OM protein - protein search, using sw model

Run on: December 7, 2005, 13:33:46 ; Search time 167 Seconds  
(without alignments)  
1718.855 Million cell updates/sec

Title: US-10-061-727-2  
Perfect score: 3669  
Sequence: 1 MTLWCVVSLYFYGIQSDA.....SALALHFTDLNNDFYIL 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Minimum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3667	99.9	687	4	US-10-061-727-2 Sequence 2, Appl
2	3281	89.4	685	4	US-10-061-727-4 Sequence 4, Appl
3	2595	70.7	822	4	US-10-167-127-16 Sequence 16, Appl
4	2586	70.5	570	4	US-10-011-548-36 Sequence 36, Appl
5	2586	70.5	570	4	US-10-167-127-10 Sequence 10, Appl
6	2580	70.3	570	4	US-10-215-211-4 Sequence 4, Appl
7	2327.5	63.4	570	4	US-10-011-548-21 Sequence 21, Appl
8	2327.5	63.4	570	4	US-10-205-219-23 Sequence 23, Appl
9	1937.5	52.8	915	4	US-10-282-162-52 Sequence 52, Appl
10	1937.5	52.8	915	5	US-10-840-138-22 Sequence 22, Appl
11	1937.5	52.8	915	5	US-10-945-068-22 Sequence 22, Appl
12	1937.5	52.8	915	6	US-11-056-730-22 Sequence 22, Appl
13	1937.5	52.8	915	6	US-11-134-114-52 Sequence 52, Appl
14	1937.5	52.8	917	4	US-10-282-162-56 Sequence 56, Appl
15	1937.5	52.8	917	4	US-10-282-162-56 Sequence 56, Appl
16	1937.5	52.8	917	5	US-10-840-138-24 Sequence 24, Appl
17	1937.5	52.8	917	5	US-10-840-138-26 Sequence 26, Appl
18	1937.5	52.8	917	5	US-10-945-068-24 Sequence 24, Appl
19	1937.5	52.8	917	5	US-10-945-068-26 Sequence 26, Appl
20	1937.5	52.8	917	6	US-11-056-730-24 Sequence 24, Appl
21	1937.5	52.8	917	6	US-11-056-730-26 Sequence 26, Appl
22	1937.5	52.8	917	6	US-11-134-114-54 Sequence 54, Appl
23	1937.5	52.8	917	6	US-11-134-114-56 Sequence 56, Appl
24	1935	52.7	359	6	US-11-096-039-4 Sequence 4, Appl
25	1935	52.7	900	4	US-10-282-162-40 Sequence 40, Appl
26	1935	52.7	900	5	US-10-840-138-10 Sequence 10, Appl
27	1935	52.7	900	5	US-10-945-068-10 Sequence 10, Appl

28	1935	52.7	900	6	US-11-056-730-10	Sequence 10, Appl
29	1935	52.7	900	6	US-11-134-114-40	Sequence 40, Appl
30	1935	52.7	902	4	US-10-282-162-42	Sequence 42, Appl
31	1935	52.7	902	4	US-10-282-162-44	Sequence 44, Appl
32	1935	52.7	902	5	US-10-840-138-12	Sequence 12, Appl
33	1935	52.7	902	5	US-10-840-138-14	Sequence 14, Appl
34	1935	52.7	902	5	US-10-945-068-12	Sequence 12, Appl
35	1935	52.7	902	5	US-10-945-068-14	Sequence 14, Appl
36	1935	52.7	902	6	US-11-056-730-12	Sequence 12, Appl
37	1935	52.7	902	6	US-11-056-730-14	Sequence 14, Appl
38	1935	52.7	902	6	US-11-134-114-42	Sequence 42, Appl
39	1935	52.7	902	6	US-11-134-114-44	Sequence 44, Appl
40	1934	52.7	359	4	US-10-215-211-6	Sequence 6, Appl
41	1930	52.6	910	3	US-09-313-942-28	Sequence 28, Appl
42	1930	52.6	910	3	US-09-935-868-28	Sequence 28, Appl
43	1930	52.6	910	4	US-10-287-035-28	Sequence 28, Appl
44	1930	52.6	910	4	US-10-282-162-28	Sequence 28, Appl
45	1930	52.6	910	5	US-10-840-138-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-061-727-2  
; Sequence 2, Application US/10061727  
; Publication No. US20030170632A1  
; GENERAL INFORMATION:  
; APPLICANT: Sims, John E.  
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN  
; FILE REFERENCE: 3151-A  
; CURRENT APPLICATION NUMBER: US/10/061,727  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: US 60/244,831  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 687  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (598)-(598)  
; OTHER INFORMATION: The 'Xaa' at location 598 stands for Thr or Pro.  
US-10-061-727-2

Query Match	99.9%	Score 3667;	DB 4;	Length 687;
Best Local Similarity	100.0%	Pred. No. 2e-311;		
Matches 687;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MTLWCVVSLYFYGIQSDASERCDWGLDMRQIQVPEDEPARIKCPLFHFHFKFNYST 60		
Db	1	MTLWCVVSLYFYGIQSDASERCDWGLDMRQIQVPEDEPARIKCPLFHFHFKFNYST 60		
Qy	61	AHSAGLTILWYTRQDRDLPEINFRIPENRISKEKVLWFRPTLLNDGNTGNTCLRNNTT 120		
Db	61	AHSAGLTILWYTRQDRDLPEINFRIPENRISKEKVLWFRPTLLNDGNTGNTCLRNNTT 120		
Qy	121	YCSKVAPLEVVQKDSFCNSPMKLPVHKLYIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180		
Db	121	YCSKVAPLEVVQKDSFCNSPMKLPVHKLYIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180		
Qy	181	CYKIQNFNNVPIEGNNLSFLIALISNNGNVYTCVVTYPENGRTEHLTRTLTKVKGSPKNA 240		
Db	181	CYKIQNFNNVPIEGNNLSFLIALISNNGNVYTCVVTYPENGRTEHLTRTLTKVKGSPKNA 240		
Qy	241	VPPVHSPNDHVVYKEKGEELLIPCTVYFSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300		
Db	241	VPPVHSPNDHVVYKEKGEELLIPCTVYFSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300		
Qy	301	SISHSRTEDETRTQILSIKKVTSBDLKRYSVCHARSASGEVAKAKQKVPAPRYTVEL 360		

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Db 301 SISHRTEDTRTQILSIKKVTSSEDLKRSVYCHARSAGKGEVAKAAKVKQVPAPRYTVEL 360
Qy 361 ACGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 420
Db 361 ACGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 420
Qy 421 VLLTGLRVLENEFGYKLCIFDRDSLPGNTVEAFDFIQRSRMIVVLSPDYVTEKISM 480
Db 421 VLLTGLRVLENEFGYKLCIFDRDSLPGNTVEAFDFIQRSRMIVVLSPDYVTEKISM 480
Qy 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPIGLQLKESVSVSWKGEKSKHSGSKFWKAL 540
Db 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPIGLQLKESVSVSWKGEKSKHSGSKFWKAL 540
Qy 541 RLALPLRSLSASSGWNESCSSQSDISLDHVQRRSRRLKEPPELOSSERAAGSPAPGXMS 600
Db 541 RLALPLRSLSASSGWNESCSSQSDISLDHVQRRSRRLKEPPELOSSERAAGSPAPGXMS 600
Qy 601 KHRGKSATRCCTVYCEGENHLNRKSRABEIHNPQWETHLCKPVPQSESTQWIONGTRL 660
Db 601 KHRGKSATRCCTVYCEGENHLNRKSRABEIHNPQWETHLCKPVPQSESTQWIONGTRL 660
Qy 661 EPPAPQISALALHHFTDLSNNDFYIL 687
Db 661 EPPAPQISALALHHFTDLSNNDFYIL 687
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## RESULT 2

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US-10-061-727-4
; Sequence 4, Application US/10061727
; Publication No. US20030170632A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, John E.
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
; FILE REFERENCE: 3151-A
; CURRENT APPLICATION NUMBER: US/10/061,727
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,831
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-061-727-4
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Query Match 89.4%; Score 3281; DB 4; Length 685;
Best Local Similarity 88.5%; Pred. No. 1.2e-277;
Matches 608; Conservative 39; Mismatches 38; Indels 2; Gaps 2;

Qy 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFDEDEPARIKCPLEFHLKFNYS 60
Db 1 MGLWYLSYFYGILOSASERCDDWGLDMRQIQVFDEDEPARIKCPLEFHLKFNYS 60
Qy 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISKEKDVLMFRPTLLNDTGNYTCMLRNTT 120
Db 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISKEKDVLMFRPTLLNDTGNYTCMLRNTT 120
Qy 121 YCSKVAAPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180
Db 121 YCSKVAAPLEVVQKDSCFNSAMRPPVHKMIEHGIKHTICPNVDGVPSSVKPSVTWYKG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTPHLLTRTLTKVVGSPKNA 240
Db 181 CTEIVDPHNLVPEGMNLSFLIPLVSNNGNYTCVVYPENGRTPHLLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYVEKPEGELLIPCTVYFSLMDSRNEVWWTIDGKKPDDITIDVTINE 300
Db 241 LPQIYSPNDRVVYVEKPEGELVIPCXYFSLMDSHNEVWWTIDGKKPDDVTDVTINE 300
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Qy 301 SISHRTEDTRTQILSIKKVTSSEDLKRSVYCHARSAGKGEVAKAAKVKQVPAPRYTVEL 360
Db 301 SVSYSTEDTRTQILSIKKVTPEDLRNRYVCHARNTKGEAQAAKVKQVIPPRYTVEL 360
Qy 361 ACGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 420
Db 361 ACGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 420
Qy 421 VLLTGLRVLENEFGYKLCIFDRDSLPGNTVEAFDFIQRSRMIVVLSPDYVTEKISM 480
Db 421 VLLTGLRVLENEFGYKLCIFDRDSLPGNTVEAFDFIQRSRMIVVLSPDYVTEKISM 480
Qy 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPIGLQLKESVSVSWKGEKSKHSGSKFWKAL 540
Db 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPIGLQLKESVSVSWKGEKSKHSGSKFWKAL 540
Qy 541 RLALPLRSLSASSGWNESCSSQSDISLDHVQRRSRRLKEPPELOSSERAAGSPAPGXMS 600
Db 541 RLALPLRSLSASSGWNESCSSQSDISLDHVQRRSRRLKEPPELOSSERAAGSPAPGXMS 599
Qy 601 KHRGKSATRCCTVYCEGENHLNRKSRABEIHNPQWETHLCKPVPQSESTQWIONGTRL 660
Db 600 KHRGKPSAACRCCTVYCEGESHLRSKRAEMTHPQWETHLCKPPLQESSESMIONGTRP 659
Qy 661 EPPAPQISALALHHFTDLSNNDFYIL 687
Db 660 E-PAPQISALALRHFTDLSNNDFYIL 685

RESULT 3
US-10-167-127-16
; Sequence 16, Application US/10167127
; Publication No. US20030100031A1
; GENERAL INFORMATION:
; APPLICANT: DOWER, STEVEN
; APPLICANT: DUFF, GORDON W.
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY
; FILE REFERENCE: MSA-026.01 (20974-2601)
; CURRENT APPLICATION NUMBER: US/10/167,127
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/297,305
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-127-16
```

```
Query Match 70.7%; Score 2595; DB 4; Length 822;
Best Local Similarity 82.1%; Pred. No. 1.7e-217;
Matches 499; Conservative 36; Mismatches 45; Indels 28; Gaps 7;

Qy 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFDEDEPARIKCPLEFHLKFNYS 60
Db 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFDEDEPARIKCPLEFHLKFNYS 60
Qy 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISKEKDVLMFRPTLLNDTGNYTCMLRNTT 120
Db 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISKEKDVLMFRPTLLNDTGNYTCMLRNTT 120
Qy 121 YCSKVAAPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180
Db 121 YCSKVAAPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTPHLLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTPHLLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYVEKPEGELLIPCTVYFSLMDSRNEVWWTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYVEKPEGELLIPCTVYFSLMDSRNEVWWTIDGKKPDDITIDVTINE 300
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Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKDDITIDVTINE 300  
Qy 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAAVKQVPAPRYTVEL 360  
Db 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAAVKQVPAPRYTVEL 360  
Qy 361 ACGFGATVLLVILVYVHYVWLEMLVLYRAHFGTDETLIDGKEYDIYVSYARNAEEBEF 420  
Db 361 ACGFGATVLLVILVYVHYVWLEMLVLYRAHFGTDETLIDGKEYDIYVSYARNAEEBEF 420  
Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVAVDFIORSRRMIVLSPDYVTEKSIISM 480  
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVAVDFIORSRRMIVLSPDYVTEKSIISM 480  
Qy 481 LEFKLGVMCQNSIATK---LIVVEYRPLEHPHPIQLQKES---VSFVSWKGEKSKHSG 533  
Db 481 LELKAGL---ENMASRGNINVLVQYKAVKETK--VKELKRAKTVLTVIKWGEKSKYPQ 535  
Qy 534 SKFWKALRLALPURLSASSGWNESCOSQDISLDHVORRRRLKEPPELOSSERAAGSP 593  
Db 536 GRFWKQLQVAMPVKKSPRESSDDEQGLSYS--SLKNVGR-----VPP-----ARDP 579  
Qy 594 PAPGXMSK 601  
Db 580 PVATMVSK 587

RESULT 4

US-10-011-548-36  
; Sequence 36, Application US/10011548  
; Publication No. US20030055218A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; Debets, Johannes Eduard Maria  
; Antonius  
; Sana, Theodore R.  
; Bazan, J. Fernando  
; Kastelein, Robert A.  
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and  
; Methods  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/011,548  
; FILING DATE: 22-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/173,151  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 60/065,776  
; FILING DATE: 17-NOV-1997  
; APPLICATION NUMBER: US 60/078,008  
; FILING DATE: 12-MAR-1998  
; APPLICATION NUMBER: US 60/081,883  
; FILING DATE: 15-APR-1998  
; APPLICATION NUMBER: US 60/095,987  
; FILING DATE: 10-AUG-1998  
; APPLICATION NUMBER: US 60/078,416  
; FILING DATE: 18-MAR-1998  
; APPLICATION NUMBER: US 60/062,066  
; FILING DATE: 15-OCT-1997  
; ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0767X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 570 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. US20030055218A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-10-011-548-36  
  
Query Match 70.5%; Score 2586; DB 4; Length 570;  
Best Local Similarity 85.3%; Pred. No. 6,1e-217;  
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;  
  
Qy 1 MTLWCVVSLYFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
Db 1 MTLWCVVSLYFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
  
Qy 61 AHSAGLTLLIWTWTRQDRDLBEPINFRLPENRISKEKVLWFRPTLLNDTGNVTCMLRNTT 120  
Db 61 AHSAGLTLLIWTWTRQDRDLBEPINFRLPENRISKEKVLWFRPTLLNDTGNVTCMLRNTT 120  
  
Qy 121 YCSKVAPELVVQKSCFNSPKMLPVHKLXIYEYGIQRITCPNVGDFYFSSVKPTITWYMG 180  
Db 121 YCSKVAPELVVQKSCFNSPKMLPVHKLXIYEYGIQRITCPNVGDFYFSSVKPTITWYMG 180  
  
Qy 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVVGSPKNA 240  
Db 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVVGSPKNA 240  
  
Qy 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKDDITIDVTINE 300  
Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKDDITIDVTINE 300  
  
Qy 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAAVKQVPAPRYTVEL 360  
Db 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAAVKQVPAPRYTVEL 360  
  
Qy 361 ACGFGATVLLVILVYVHYVWLEMLVLYRAHFGTDETLIDGKEYDIYVSYARNAEEBEF 420  
Db 361 ACGFGATVLLVILVYVHYVWLEMLVLYRAHFGTDETLIDGKEYDIYVSYARNAEEBEF 420  
  
Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVAVDFIORSRRMIVLSPDYVTEKSIISM 480  
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVAVDFIORSRRMIVLSPDYVTEKSIISM 480  
  
Qy 481 LEFKLGVMCQNSIATK---LIVVEYRPLEHPHPIQLQKES---VSFVSWKGEKSKHSG 533  
Db 481 LELKAGL---ENMASRGNINVLVQYKAVKETK--VKELKRAKTVLTVIKWGEKSKYPQ 535  
  
Qy 534 SKFWKALRLALPURLSASSGWNESCOSQDISLDHVORRRRLKEPPELOSSERAAGSP 593  
Db 536 GRFWKQLQVAMPVKKSPRESSDDEQGLSYS--SLKNVGR-----VPP-----ARDP 579  
  
RESULT 5  
US-10-167-127-10  
; Sequence 10, Application US/10167127  
; Publication No. US20030100031A1  
; GENERAL INFORMATION:  
; APPLICANT: DOWE, STEVEN  
; APPLICANT: DUFF, GORDON W.  
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY  
; TITLE REFERENCE: MSA-026.01 (20974-2601)  
; FILE REFERENCE: MSA-026.01 (20974-2601)  
; CURRENT APPLICATION NUMBER: US/10/167,127  
; CURRENT FILING DATE: 2002-06-11

```
; PRIOR APPLICATION NUMBER: 60/297,305
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-127-10

Query Match          70.5%; Score 2586; DB 4; Length 570;
Best Local Similarity 85.3%; Pred. No. 6.1e-217;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

Qy 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEHFLKFNYS 60
Db 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEHFLKFNYS 60

Qy 61 AHSAGLTLIYWTRQDRDLLEEPINFRLENRISEKEDVLMFRPTLLNDTNGYTCMLRNT 120
Db 61 AHSAGLTLIYWTRQDRDLLEEPINFRLENRISEKEDVLMFRPTLLNDTNGYTCMLRNT 120

Qy 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQRIICPNVDGYFPSSVKPTITWYG 180
Db 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQRIICPNVDGYFPSSVKPTITWYG 180

Qy 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTPHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTPHLTRTLTKVVGSPKNA 240

Qy 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSFLMDSRNEVWTTIDGKKPDDITIDVTINE 300
Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSFLMDSRNEVWTTIDGKKPDDITIDVTINE 300

Qy 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAOKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAOKVPAPRYTVEL 360

Qy 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAESEEF 420
Db 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAESEEF 420

Qy 421 VLLTLRGVLENEFGYKLCIFDRSLPGCNTVEAFDFIQRSMRIMVLSYDYVTEKISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRSLPGGI VTDFTLSFIQSRRLVLSYVYLQGTQAL 480

Qy 481 LEFKLGVMCQNSIATK----LVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSG 533
Db 481 LEFKLGVMCQNSIATK----LVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSG 533

Qy 534 SKFWKALRLALPLRSLSASSGMNESCSSQSDI 565
Db 536 GFEWKQLQVAMPVKSPRRSSDEQGLSYSSL 567

RESULT 6
US-10-215-211-4
; Sequence 4, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 570
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-215-211-4

Query Match          70.3%; Score 2580; DB 4; Length 570;
Best Local Similarity 85.6%; Pred. No. 2.1e-216;
Matches 487; Conservative 31; Mismatches 45; Indels 6; Gaps 3;

Qy 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEHFLKFNYS 60
Db 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEHFLKFNYS 60

Qy 61 AHSAGLTLIYWTRQDRDLLEEPINFRLENRISEKEDVLMFRPTLLNDTNGYTCMLRNT 120
Db 61 AHSAGLTLIYWTRQDRDLLEEPINFRLENRISEKEDVLMFRPTLLNDTNGYTCMLRNT 120

Qy 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQRIICPNVDGYFPSSVKPTITWYG 180
Db 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQRIICPNVDGYFPSSVKPTITWYG 180

Qy 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTPHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTPHLTRTLTKVVGSPKNA 240

Qy 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSFLMDSRNEVWTTIDGKKPDDITIDVTINE 300
Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSFLMDSRNEVWTTIDGKKPDDITIDVTINE 300

Qy 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAOKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAOKVPAPRYTVEL 360

Qy 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAESEEF 420
Db 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAESEEF 420

Qy 421 VLLTLRGVLENEFGYKLCIFDRSLPGCNTVEAFDFIQRSMRIMVLSYDYVTEKISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRSLPGGI VTDFTLSFIQSRRLVLSYVYLQGTQAL 480

Qy 481 LEFKLGVMCQNSIATK----LVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSG 536
Db 481 LEFKLGVMCQNSIATK----LVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSG 536

Qy 537 WKALRLALPLRSLSASSGMNESCSSQSDI 565
Db 539 WKQLQVAMPVKSPRRSSDEQGLSYSSL 567

RESULT 7
US-10-011-548-21
; Sequence 21, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; METHODS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/011,548  
 FILING DATE: 22-Oct-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/173,151  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 60/065,776  
 FILING DATE: 17-NOV-1997  
 APPLICATION NUMBER: US 60/078,008  
 FILING DATE: 12-MAR-1998  
 APPLICATION NUMBER: US 60/081,883  
 FILING DATE: 15-APR-1998  
 APPLICATION NUMBER: US 60/095,987  
 FILING DATE: 10-AUG-1998  
 APPLICATION NUMBER: US 60/078,416  
 FILING DATE: 18-MAR-1998  
 APPLICATION NUMBER: US 60/062,066  
 FILING DATE: 15-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0767X  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650)852-9196  
 TELEFAX: (650)496-1200  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 570 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: No. US20030055218A1 Relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Query Match 63.4%; Score 2327.5; DB 4; Length 570;  
 Best Local Similarity 75.9%; Pred. No. 2.6e-194;  
 Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

QY 1 MTLWCVVSLFYGILOSDASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
 DB 1 MGLLWYLSLFSYGILOSHASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
 QY 61 AHSAGLTLIWWTQRDRLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120  
 DB 61 AHSAGLTLIWWTQRDRLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120  
 QY 121 YCSKVAFFLEVQKDSFCNSPMKLPVHKLYIEYGIORITCPNVGYPFSSVKPPTITWYMG 180  
 DB 121 YCSKVAFFLEVQKDSFCNSAMRFPVHKMYIEHGHKITCPNVGYPFSSVKPSTWYKG 180  
 QY 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTPHLTRTLTVKVVGSPKNA 240  
 DB 181 CTEIVDFHNLVPEGNNLSFFIPLVSNNGNYTCVVTYPENGRLEHLTRTVTVKVVGSPKDA 240  
 QY 241 VPPVHSPNDHVYKEKEGELLIPCTVYFSLMDSRNEVWMTIDGKPPDITTDVTINE 300  
 DB 241 LPPQIYSNDRVYKEKEGELLVPCVYFSDSHNEVWMTIDGKPPDVTVDITINE 300  
 QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGKAEVAKVKQKVPAPRYTVEL 360  
 DB 301 SVSYSSSTEDETRTQILSIKKVTPEDLRNRYVCHARNTKGEAEQAQKVKQKVPAPRYTVEL 360  
 QY 361 ACGFATVLLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEF 420  
 DB 361 ACGFATVFLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEF 420  
 QY 421 VLLTLRGVLENEFGYKLCIFDRDSLPGCNTVEAFDFIQRSRMIVLSPDYVTEKSTISM 480  
 DB 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLISFIQSRRLVVLSPNYVLQGTQAL 480  
 QY 481 LEFLKLVGMVCONSIATK----LIVVEYRPLEHPHGPILQLKES---VSFVSWKGEKSKHSG 533

QY 481 LEFLKLVGMVCONSIATK----LIVVEYRPLEHPHGPILQLKES---VSFVSWKGEKSKHSG 533  
 DB 481 LELKAGL---EMASRGNINVLVOYKAVKDMK--VKELKRAKTVLTWIKWGEKSKYPQ 535  
 QY 534 SKFWKALRLALPLRSLSASSGWNES 558  
 DB 536 GRFWKQLQVAMPVKK---SPRWSSN 557

RESULT 8  
 US-10-205-219-23  
 ; Sequence 23, Application US/10205219  
 ; Publication No. US20030138803A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warner-Lambert Company  
 ; APPLICANT: Lee, Kevin  
 ; APPLICANT: Dixon, Alistair  
 ; APPLICANT: Brookabank, Robert  
 ; APPLICANT: Pinnock, Robert  
 ; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
 ; FILE REFERENCE: WL-A-018200  
 ; CURRENT APPLICATION NUMBER: US/10/205,219  
 ; CURRENT FILING DATE: 2002-07-24  
 ; PRIOR APPLICATION NUMBER: GB 0118354.0  
 ; PRIOR FILING DATE: 2001-07-27  
 ; NUMBER OF SEQ ID NOS: 197  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 23  
 ; LENGTH: 570  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; OTHER INFORMATION: Second subunit of the interleukin 1 receptor complex  
 US-10-205-219-23

Query Match 63.4%; Score 2327.5; DB 4; Length 570;  
 Best Local Similarity 75.9%; Pred. No. 2.6e-194;  
 Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

QY 1 MTLWCVVSLFYGILOSDASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
 DB 1 MGLLWYLSLFSYGILOSHASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
 QY 61 AHSAGLTLIWWTQRDRLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120  
 DB 61 AHSAGLTLIWWTQRDRLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120  
 QY 121 YCSKVAFFLEVQKDSFCNSPMKLPVHKLYIEYGIORITCPNVGYPFSSVKPPTITWYMG 180  
 DB 121 YCSKVAFFLEVQKDSFCNSAMRFPVHKMYIEHGHKITCPNVGYPFSSVKPSTWYKG 180  
 QY 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTPHLTRTLTVKVVGSPKNA 240  
 DB 181 CTEIVDFHNLVPEGNNLSFFIPLVSNNGNYTCVVTYPENGRLEHLTRTVTVKVVGSPKDA 240  
 QY 241 VPPVHSPNDHVYKEKEGELLIPCTVYFSLMDSRNEVWMTIDGKPPDITTDVTINE 300  
 DB 241 LPPQIYSNDRVYKEKEGELLVPCVYFSDSHNEVWMTIDGKPPDVTVDITINE 300  
 QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGKAEVAKVKQKVPAPRYTVEL 360  
 DB 301 SVSYSSSTEDETRTQILSIKKVTPEDLRNRYVCHARNTKGEAEQAQKVKQKVPAPRYTVEL 360  
 QY 361 ACGFATVLLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEF 420  
 DB 361 ACGFATVFLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEF 420  
 QY 421 VLLTLRGVLENEFGYKLCIFDRDSLPGCNTVEAFDFIQRSRMIVLSPDYVTEKSTISM 480  
 DB 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLISFIQSRRLVVLSPNYVLQGTQAL 480  
 QY 481 LEFLKLVGMVCONSIATK----LIVVEYRPLEHPHGPILQLKES---VSFVSWKGEKSKHSG 533

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Db 481 LELKAGL---ENMASRGNINVLQYKAVKDMK--VKELKRAKTVLTIVIKWKGSKYKYPQ 535
Qy 534 SKFWALRLALPLRLSLSSASSGWNES 558
Db 536 GRFWKQLQVAMPVKK---SPRWSSN 557

RESULT 9
US-10-282-162-52
; Sequence 52, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282.162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-52

Query Match 52.8%; Score 1937.5; DB 4; Length 915;
Best Local Similarity 80.9%; Pred. No. 7.3e-160;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSVSLYFYGILOSASERCDDWGLDTRMQIQVFEDEPARIKCPLEHFLKFNYS 60
Db 1 MVLWCVSVSLYFYGILOSASERCDDWGLDTRMQIQVFEDEPARIKCPLEHFLKFNYS 60
Qy 61 AHSAGLTLIYWTRQDRDLSEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLSEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Db 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Db 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVILIVVHVWLEMLVIFYRAHF----- 393
Db 361 GAARSCFRGRHYKREFRLEGEPAVLRCPQV----PYWLWASVSPRINLTWKNDSARTV 416
Qy 394 -GTDETL----DG-----KEYDIYVSYARNABEEFVLLTLRGVLN 431
Db 417 PGSEETRMWAQDGMALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 10
US-10-840-138-22
; Sequence 22, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
```

```
; APPLICANT: Lin, Hsin Chieh
; APPLICANT: Karow, Margaret
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840.138
; CURRENT FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-840-138-22
```

```
Query Match 52.8%; Score 1937.5; DB 5; Length 915;
Best Local Similarity 80.9%; Pred. No. 7.3e-160;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSVSLYFYGILOSASERCDDWGLDTRMQIQVFEDEPARIKCPLEHFLKFNYS 60
Db 1 MVLWCVSVSLYFYGILOSASERCDDWGLDTRMQIQVFEDEPARIKCPLEHFLKFNYS 60
Qy 61 AHSAGLTLIYWTRQDRDLSEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLSEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Db 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Db 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVILIVVHVWLEMLVIFYRAHF----- 393
Db 361 GAARSCFRGRHYKREFRLEGEPAVLRCPQV----PYWLWASVSPRINLTWKNDSARTV 416
Qy 394 -GTDETL----DG-----KEYDIYVSYARNABEEFVLLTLRGVLN 431
Db 417 PGSEETRMWAQDGMALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466
```

```
RESULT 11
US-10-945-068-22
; Sequence 22, Application US/10945068
; Publication No. US20050129685A1
; GENERAL INFORMATION:
; APPLICANT: Jingtai Cao
; APPLICANT: Stanley J. Wiegand
; TITLE OF INVENTION: USE OF IL-1 BLOCKERS TO PREVENT CORNEAL INFLAMMATION
; FILE REFERENCE: REG 208A
; CURRENT APPLICATION NUMBER: US/10/945.068
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/503.854
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-945-068-22
```



Query Match 52.8%; Score 1937.5; DB 5; Length 915;  
Best Local Similarity 80.9%; Pred. No. 7.3e-160;  
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

QY 1 MTLWCVSLYFYGILQSDASERCDDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
DB 1 MVLWCVSLYFYGILQSDASERCDDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGLTLIWYTRQDRDLEEPINFRLPENRISKEKDVLMWFRPTLLNDTGNVTCMLRNTT 120  
DB 61 AHSAGLTLIWYTRQDRDLEEPINFRLPENRISKEKDVLMWFRPTLLNDTGNVTCMLRNTT 120

QY 121 YCSKVAFFLEVVQKSCFNPKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180  
DB 121 YCSKVAFFLEVVQKSCFNPKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180

QY 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240  
DB 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPTCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300  
DB 241 VPPVHSPNDHVYKEPGEELLIPTCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSIDLKRSYVCHARSAGEVAKAAKVKQVPAPRYTVHT 360  
DB 301 SISHSRTEDETRTQILSIKKVTSIDLKRSYVCHARSAGEVAKAAKVKQVPAPRYTVHT 360

QY 361 ----ACGF-----GATVLLWLIVVYHVYVLEWLVFYRAHF----- 393  
DB 361 GAASCRFRGRHYKREFLEGPVALRCPQV-----PYLWASVSPRINLTWHKNDARSATV 416

QY 394 -CTDETL---DG-----KEYDIYVSYARNAEFEFVLLTLRGVLEN 431  
DB 417 PGEETRMAQDGLWLLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 12  
US-11-056-730-22  
; Sequence 22, Application US/11056730  
; Publication No. US20050197293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mellie, Scott  
; APPLICANT: Stahl, Neil  
; APPLICANT: Radin, Allen  
; APPLICANT: Weinstein, Steven  
; APPLICANT: Calaprice, Denise  
; APPLICANT: Karow, Margaret  
; APPLICANT: Papadopoulos, Joanne  
; TITLE OF INVENTION: Use of an IL-1 Antagonist for Treating Arthritis  
; FILE REFERENCE: 203G  
; CURRENT APPLICATION NUMBER: US/11/056,730  
; CURRENT FILING DATE: 2005-02-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 915  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-056-730-22

Query Match 52.8%; Score 1937.5; DB 6; Length 915;  
Best Local Similarity 80.9%; Pred. No. 7.3e-160;  
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

QY 1 MTLWCVSLYFYGILQSDASERCDDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
DB 1 MVLWCVSLYFYGILQSDASERCDDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGLTLIWYTRQDRDLEEPINFRLPENRISKEKDVLMWFRPTLLNDTGNVTCMLRNTT 120

DB 61 AHSAGLTLIWYTRQDRDLEEPINFRLPENRISKEKDVLMWFRPTLLNDTGNVTCMLRNTT 120  
QY 121 YCSKVAFFLEVVQKSCFNPKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180  
DB 121 YCSKVAFFLEVVQKSCFNPKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180

QY 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240  
DB 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPTCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300  
DB 241 VPPVHSPNDHVYKEPGEELLIPTCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSIDLKRSYVCHARSAGEVAKAAKVKQVPAPRYTVHT 360  
DB 301 SISHSRTEDETRTQILSIKKVTSIDLKRSYVCHARSAGEVAKAAKVKQVPAPRYTVHT 360

QY 361 ----ACGF-----GATVLLWLIVVYHVYVLEWLVFYRAHF----- 393  
DB 361 GAASCRFRGRHYKREFLEGPVALRCPQV-----PYLWASVSPRINLTWHKNDARSATV 416

QY 394 -GTDETL---DG-----KEYDIYVSYARNAEFEFVLLTLRGVLEN 431  
DB 417 PGEETRMAQDGLWLLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 13  
US-11-134-114-52  
; Sequence 52, Application US/11134114  
; Publication No. US20050222033A1  
; GENERAL INFORMATION:  
; APPLICANT: Stahl, Neil  
; APPLICANT: Yancopoulos, George D.  
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using  
; FILE REFERENCE: 203C1  
; CURRENT APPLICATION NUMBER: US/11/134,114  
; CURRENT FILING DATE: 2005-05-20  
; PRIOR APPLICATION NUMBER: 10/282,162  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 09/313,942  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/101,858  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 52  
; LENGTH: 915  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-134-114-52

Query Match 52.8%; Score 1937.5; DB 6; Length 915;  
Best Local Similarity 80.9%; Pred. No. 7.3e-160;  
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

QY 1 MTLWCVSLYFYGILQSDASERCDDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60  
DB 1 MVLWCVSLYFYGILQSDASERCDDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGLTLIWYTRQDRDLEEPINFRLPENRISKEKDVLMWFRPTLLNDTGNVTCMLRNTT 120  
DB 61 AHSAGLTLIWYTRQDRDLEEPINFRLPENRISKEKDVLMWFRPTLLNDTGNVTCMLRNTT 120

QY 121 YCSKVAFFLEVVQKSCFNPKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180  
DB 121 YCSKVAFFLEVVQKSCFNPKLPVHKLYIEYGIQRIITCPNVGDFPSSVKPTITWYMG 180

QY 181 CYKIQNFNNVPIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240

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Db 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVGSPKNA 240
Qy 241 VPPVIHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTVHT 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVVLIVVHVWLEWLVFYRAHF----- 393
Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARTV 416
Qy 394 -GTDETIL----DG-----KEYDIYVSYARNAEEEEFFVLLTLRGLVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 14
US-10-282-162-54
; Sequence 54, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-54

Query Match 52.8%; Score 1937.5; DB 4; Length 917;
Best Local Similarity 80.9%; Pred. No. 7.3e-150;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Db 1 MVLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLWFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLWFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Db 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVGSPKNA 240
Db 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVGSPKNA 240
Qy 241 VPPVIHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTVHT 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVVLIVVHVWLEWLVFYRAHF----- 393
Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARTV 416
Qy 394 -GTDETIL----DG-----KEYDIYVSYARNAEEEEFFVLLTLRGLVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

Search completed: December 7, 2005, 13:47:02
Job time : 170 secs
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Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARTV 416
Qy 394 -GTDETIL----DG-----KEYDIYVSYARNAEEEEFFVLLTLRGLVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 15
US-10-282-162-56
; Sequence 56, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-56

Query Match 52.8%; Score 1937.5; DB 4; Length 917;
Best Local Similarity 80.9%; Pred. No. 7.3e-160;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Db 1 MVLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLWFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLWFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Db 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVGSPKNA 240
Db 181 CYKIQNFNNVPIEGMNLISFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVGSPKNA 240
Qy 241 VPPVIHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTVHT 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVVLIVVHVWLEWLVFYRAHF----- 393
Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARTV 416
Qy 394 -GTDETIL----DG-----KEYDIYVSYARNAEEEEFFVLLTLRGLVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

Search completed: December 7, 2005, 13:47:02
Job time : 170 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 7, 2005, 13:34:02 ; Search time 12 Seconds  
(without alignments)  
319.708 Million cell updates/sec

Title: US-10-061-727-2  
Perfect score: 3669  
Sequence: 1 MTLWCVVSLFYGIQSDA.....SALAHHTDLSNNDFVIL 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	252	6.9	398	6	US-10-821-234-1583
2	148	4.0	7968	7	US-11-186-731-5
3	130	3.5	1049	6	US-10-131-826A-358
4	121	3.3	879	7	US-11-022-562-340
5	121	3.3	1338	6	US-10-821-234-1622
6	115	3.1	1338	7	US-11-109-156-23
7	111	3.0	1119	6	US-10-131-826A-352
8	109	3.0	583	7	US-11-080-991-64
9	108	2.9	532	7	US-11-104-812-2
10	106	2.9	532	7	US-11-105-279-2
11	106	2.9	567	7	US-11-016-503-10
12	106	2.9	2828	7	US-11-080-991-54
13	106	2.9	2828	7	US-11-186-284-49
14	105	2.9	1694	7	US-11-135-855-36
15	105	2.9	1709	7	US-11-135-855-35
16	103	2.8	567	7	US-11-016-503-2
17	101	2.8	1032	7	US-11-014-367-2
18	100	2.7	4419	6	US-10-821-234-1155
19	98.5	2.7	455	7	US-11-016-503-14
20	98.5	2.7	455	7	US-11-089-803-4
21	97.5	2.7	409	6	US-10-821-234-892
22	97	2.6	557	7	US-11-016-503-4
23	97	2.6	985	7	US-11-113-424-61
24	96.5	2.6	1250	7	US-11-137-465-62
25	95	2.6	462	7	US-11-016-503-8

26	94.5	2.6	740	7	US-11-137-465-61	Sequence 61, Appl
27	94	2.6	1897	6	US-10-821-234-1635	Sequence 1635, Ap
28	94	2.6	1907	7	US-11-000-463-250	Sequence 250, App
29	92.5	2.5	300	7	US-11-025-834A-21	Sequence 21, Appl
30	92.5	2.5	649	7	US-11-102-240-132	Sequence 132, App
31	92.5	2.5	1032	7	US-11-014-367-3	Sequence 3, Appl
32	91.5	2.5	326	6	US-10-999-866-36	Sequence 36, Appl
33	91.5	2.5	326	7	US-11-144-248-28	Sequence 28, Appl
34	91.5	2.5	326	7	US-11-061-821-36	Sequence 36, Appl
35	91.5	2.5	470	7	US-11-144-248-45	Sequence 45, Appl
36	91.5	2.5	470	7	US-11-144-248-46	Sequence 46, Appl
37	91.5	2.5	470	7	US-11-144-248-49	Sequence 49, Appl
38	91.5	2.5	473	7	US-11-144-248-50	Sequence 50, Appl
39	91.5	2.5	983	7	US-11-113-424-59	Sequence 59, Appl
40	91	2.5	450	6	US-10-131-826A-378	Sequence 378, App
41	90.5	2.5	450	7	US-11-025-712-12	Sequence 12, Appl
42	90.5	2.5	477	6	US-10-131-826A-50	Sequence 50, Appl
43	90.5	2.5	628	7	US-11-080-991-108	Sequence 108, App
44	90.5	2.5	1032	6	US-10-835-475-1	Sequence 1, Appl
45	90.5	2.5	1032	7	US-11-014-367-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-10-821-234-1583  
; Sequence 1583, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821.234  
; PRIOR FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1583  
; LENGTH: 398  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-821-234-1583

Query Match	6.9%	Score 252;	DB 6;	Length 398;
Best Local Similarity	23.4%	Pred. No. 4e-15;		
Matches	79;	Conservative	51;	Mismatches 148; Indels 60; Gaps 13;
Qy	20	ASERCDWGLDMQIQVFEDEPARIKCPLEHFKFNYSHTAHAGLTLIYWTQRDL	79	
Db	24	AASRCRGRGHRKREFRL-EGEPVALRCQPVYWLWASVSPR- - - - -INLTHKQDSARTV	78	
Qy	80	--BEPINFRLEPNRISKEKDVLPFRPTLLNDTGNVTCMLNNTTYCSKVAFPLEVYVQKDC	137	
Db	79	PGEE- - - - -ETRMWAQDQALMLLPALQEDSGYVCTTRNASYCDKMSIELRVFNTDA	131	
Qy	138	FNSPMKLPVHKLYEY- - - - -GIQRITCPNVVDGYPSSVKPTITWYNGCYKIQNFN	188	
Db	132	F- - - - -LP- - - - -FISYPQILTLSTSGV- - - - -LVCPDLSEFRDKTDVKIQWKDLSLLDKDN	180	
Qy	189	NVPEGNLFLI- - - - -ALISNNGNYTCVTPENGRTFHLTRTLTVKVGSPKNAVPVI	245	
Db	181	EKFLSVRGTTLLVHDVALEDAGYRCVLTFAHEGQQVNIITRSIELRIKKKEETI- - - - -PVI	239	
Qy	246	HSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVMTIDGKKPDDITDVTINESISHS	305	
Db	240	ISPUKTI- - - - -SASLSRLTIPCKVFLGTPLTTLMTAN- - - - -DTHISSAYPGG	288	
Qy	306	RTEDETRTQI- - - - -LSIKKVTSEDLKRSYVC	332	





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Qy 433 FGYKLCIFDRDLSLPGGNTVEAVDFIQBS-----RRMIVVLSDDYVTEKSIIMLEFKLGM- 488
Db 833 LG-----RGAF--GKVQASAFGIKKSPCTRTVAVKMLKEGATASEYKALMTLKILT 883
Qy 489 -----CONSIATKLIWEX-----RPLEHPHGILQKESVSFVSKGE 527
Db 884 HIGHHLNVNLLGACTKGGPLMVIVEYCKYGNLSVLYKSKRDLFFLNKDALHMEPKKE 943
Qy 528 KSKHSGSKFWKALRLALPLRLSLS--ASSGWNESCSQSDISLDHVORRRSR--LKEP 580
Db 944 KWE--PGLSEQKKPLDLSVTSSESFASGFG-----QEDKSLSDVEEEDSDGFYKEP 993

RESULT 6
US-11-109-156-23
; Sequence 23, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-Ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-Ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-23

Query Match 3.1%; Score 115; DB 7; Length 1338;
Best Local Similarity 20.5%; Pred. No. 0.038;
Matches 136; Conservative 68; Mismatches 199; Indels 262; Gaps 34;

Qy 108 DTGNYTCML-----RNTTYCSKVAFFLEVQKD--SCFNSPMKLPVHKLYI-----EYG 154
Db 399 DAGNYTLLSIKNSQNFUKLATALIUNVKPQIYEKAVSSPDPAIPLGSRQILTCTAYG 458
Qy 155 IQRITCNVDGYPSSVVKPTITWY-----MGCYKI 184
Db 459 IP-----OPTIKFWHPCHNHSEARCDPCSNNEESFILDADSNMG-NRI 502
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Qy 185 QNFNN--VIPEGNN--LSFLIALISN--NGNYTCVVVYPENGRTPHLTRLTLTKVVGSPKN 239
Db 503 ESITORMAITEGKNKMASTLWADSRISGIYICIASN-----KVGTVG--RN 547
Qy 240 AVPPVIHSPND--HVVYEKEP--GEELIIPCTVVFSLMDSRNEVWV---TIDCK----- 287
Db 548 ISFYITDVPNGFHNLEKMPTEGEDDLKSLCTVN--KFLY-----RDVTWILLRTVNNRTWHYS 603
Qy 288 -----KPDDITIDVTI--NESISHSRT-----EDETRTOILSIKKVTSIDLKRSYV 331
Db 604 ISKQKMAITKEHSITLNLTIMNVSLQDSGYACRARNVYTGEILQKKEITIRDOEAPYL 663
Qy 332 -----CHARSAGEVAKAAVKQKVPAPRYT-----VELAC 362
Db 664 LRNLSDHTVAISSSTTLDCHANG-----VPEPOITWFKNNHKIQQEPGIL 709
Qy 363 GFGATVLLVILIV---VHVYVWLEMLVFRAPHGCTDETILDGKEYDIYVSYARNAEEE 418
Db 710 GPGSSTLFIERTVEDEGVYHCK-----ATNQK--GSVSSAYLTVGQTSDKS 755
Qy 419 EFVLLTL-----RGVLENEFGYKLCIFDRDLSL----- 446
Db 756 NLELITLTCTCVAATLFWLLLTLLIRKMKSSSEIKTDYLSIIMDPDEVLDEQERL PY 815
Qy 447 -----GGNTVEAVDFDIQRS-----RRMIVVLSDDYVTEKSIISML 481
Db 816 DASKWBFARERLKLKSLGRGAFGVQASAFGIKKSPCTRTVAVKMLKEGATASEYKAL 875
Qy 482 EFKLGM-----CONSIATKLIWEX-----RPLEHPHGILQKESV 519
Db 876 MTEKLITLTHIGHHLNVNLLGACTKGGPLMVIVEYCKYGNLSVLYKSKRDLFFLNKDA 935
Qy 520 SFVSWGKSKHSGKFWKALRLALPLRLSLS--ASSGWNESCSQSDISLDHVORRRSR-- 576
Db 936 LHMEPKKEKWE--PGLSEQKKPLDLSVTSSESFASGFG-----QEDKSLSDVEEEDSDG 988
Qy 577 -LKEP 580
Db 989 FYKEP 993

RESULT 7
US-10-131-826A-352
; Sequence 352, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Sherwood, Steven
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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Db	1081	-SEEDGKER-----TDFQENHCHTCKOTLERYTPNFQSY 1115
RESULT 8		
US-11-080-991-64		
; Sequence 64, Application US/11080991		
; Publication No. US20050266437A1		
; GENERAL INFORMATION:		
; APPLICANT: Veiby, Petter Ole		
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR		
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION		
; TITLE OF INVENTION: AND OVARIAN CANCER		
; FILE REFERENCE: MRI-039		
; CURRENT APPLICATION NUMBER: US/11/080,991		
; CURRENT FILING DATE: 2005-03-11		
; PRIOR APPLICATION NUMBER: US/10/176,847		
; PRIOR FILING DATE: 2002-06-21		
; NUMBER OF SEQ ID NOS: 112		
; SOFTWARE: FastSeq for Windows Version 4.0		
; SEQ ID NO 64		
; LENGTH: 583		
; TYPE: PRT		
; ORGANISM: Homo sapiens		
US-11-080-991-64		
Query Match 3.0%; Score 109; DB 7; Length 58		
Best Local Similarity 17.8%; Pred. No. 0.039;		
Matches 99; Conservative 58; Mismatches 141; Indels		
Qy	42	PARIKCPLFEHFLKFNYSTAHSAGLTLLIYWYTRQDRDLEP-----I
Db	42	PCRLDVPQNLMFCKWKY-----EKPDSGPVFI
Qy	96	KDVLWRPRLTLLDNGYTCMLRNTTYCSKVAFPLEVVQKDCSFPK
Db	81	DDPEYKDR-LNLSENYSLTISNARSIDEKRFVCMVLVTEDNVPEAPT
Qy	149	----LVIE-YGIORI-TCPNVDGYFPSSVKPTTITWYMGCYKIQNFNV
Db	140	VSKALFLETLQKLGDCISDSY-PDG-----NITWY-----RNGKVL
Qy	195	-----MNLFLIALISNGNYTCVVTY--PENGRTFHL--
Db	190	KEMDPVTQLYTMTSTLEYKTTKADIQMPFTCSVITYYGPSQKTIHSEQ
Qy	230	TVKVCVSPKNV-----PPVHSPN
Db	250	TIQVL-PPKNAIKEGDNITLKCILGNPNPPEEFYLPQGPGEIRSN
Qy	256	-----KEPGEELLIPCTV
Db	309	GDYKCSLIDKKSMIASITATVHYLDLSLSPSGEVTRQIGDALPVSCTII
Qy	269	-----YFSEL--MDSRNEYWMT-----IDG-KKPPDDITIDVTINE
Db	369	DNIRLRSSPFSFLHYQDAGNYVCETALQBEVGLKKRESLTLLIV----
Qy	313	TQLSLTKVTSDELKSYVCHAR-----SAKGEVAKAAK----
Db	416	POIKMTKTDPSGLSKTIICHVEGFPKPAIQWTTITGSGSVINQTEESP
Qy	353	APRYTVELACG-----
Db	476	SPENVTLICTAENQLERTVNSLNSAISPEHDEADEISDENREKVN
Qy	370	LVVILIVVYHVYWLEM 385
Db	536	LLLAALVAGVYVWLYM 551
RESULT 9		
US-11-104-812-2		



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; Sequence 2, Application US/11104812
; Publication No. US20050260153A1
; GENERAL INFORMATION:
; APPLICANT: CALIAS, PERICLES
; APPLICANT: COOK, GARY P.
; APPLICANT: SHIMA, DAVID T.
; APPLICANT: TURNER, DAVID I.
; APPLICANT: GANLEY, MARY A.
; TITLE OF INVENTION: FACILITATION OF IONTOPHORESIS USING CHARGED MOIETIES
; FILE REFERENCE: EYE-035D1V
; CURRENT APPLICATION NUMBER: US/11/104,812
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 60/561,601
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 60/658,819
; PRIOR FILING DATE: 2005-03-04
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-104-812-2

Query Match      2.9%; Score 108; DB 7; Length 532;
Best Local Similarity 22.3%; Pred. No. 0.042;
Matches 73; Conservative 38; Mismatches 94; Indels 122; Gaps 17;

Qy 106 LNDTGYTCLMRNTTYGSKVAFPLEVVQKDCSCFNSPMKLPVHKLYIEYGIQRTICPNVDG 165
Db 259 LNPTVTY----GNDSPSAKAS--VSVTAED-----GTQRLTCAVILG 295
Qy 166 YFPSSVKPTITWYMGCKYKQNF--NNVI-----PEGNLSFLI-----ALISNNG--- 208
Db 296 NQSOETLQTVTIY-----SFPAPNVILTKPEVSEGTETVTKCEAHPRAKVTILNGVPAQ 348
Qy 209 -----NYTCVVTYPENGRTFHLTRTLTKVVGSPKNAVPPVHSPNDHVYVEKEPGEEL 262
Db 349 PLGPRAQLLKATPEDNGRSFSCSATL--EVAGQ-----LIH-----KNQTRREL 390
Qy 263 LIPCTVYFSLMDSR-----NEVWMTIDGKKP-----DDITIDVTINESIS 303
Db 391 ----RVLYGPRLDERDCPGNWTWPENSQQTPMCQAWGNPLPELKLKDGTFPLPIGESVT 446
Qy 304 HSRTEDETRQILSIKKVTSSEDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVLACG 363
Db 447 VTR-----DLEGTYLCRARSTQGEVTR--EVTNVLSPRVEI----- 481
Qy 364 FGATVLLVILIVVYHYVWLEWLVFYR 390
Db 482 ---VIITVVAANVIMGTAGLSTYLYNR 505

RESULT 10
US-11-105-279-2
; Sequence 2, Application US/11105279
; Publication No. US20050260651A1
; GENERAL INFORMATION:
; APPLICANT: CALIAS, PERICLES
; APPLICANT: COOK, GARY P.
; APPLICANT: SHIMA, DAVID T.
; APPLICANT: ADAMIS, ANTHONY P.
; APPLICANT: NG, YIN-SHAN
; APPLICANT: ROBINSON, GREGORY S.
; APPLICANT: TURNER, DAVID I.
; APPLICANT: GANLEY, MARY A.
; TITLE OF INVENTION: ENHANCED BIOLOGICALLY ACTIVE CONJUGATES
; FILE REFERENCE: EYE-035
; CURRENT APPLICATION NUMBER: US/11/105,279
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 60/561,601
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 60/658,819

; Sequence 2, Application US/11104812
; Publication No. US20050260153A1
; GENERAL INFORMATION:
; APPLICANT: CALIAS, PERICLES
; APPLICANT: COOK, GARY P.
; APPLICANT: SHIMA, DAVID T.
; APPLICANT: TURNER, DAVID I.
; APPLICANT: GANLEY, MARY A.
; TITLE OF INVENTION: FACILITATION OF IONTOPHORESIS USING CHARGED MOIETIES
; FILE REFERENCE: EYE-035D1V
; CURRENT APPLICATION NUMBER: US/11/104,812
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 60/561,601
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 60/658,819
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-105-279-2

Query Match      2.9%; Score 108; DB 7; Length 532;
Best Local Similarity 22.3%; Pred. No. 0.042;
Matches 73; Conservative 38; Mismatches 94; Indels 122; Gaps 17;

Qy 106 LNDTGYTCLMRNTTYGSKVAFPLEVVQKDCSCFNSPMKLPVHKLYIEYGIQRTICPNVDG 165
Db 259 LNPTVTY----GNDSPSAKAS--VSVTAED-----GTQRLTCAVILG 295
Qy 166 YFPSSVKPTITWYMGCKYKQNF--NNVI-----PEGNLSFLI-----ALISNNG--- 208
Db 296 NQSOETLQTVTIY-----SFPAPNVILTKPEVSEGTETVTKCEAHPRAKVTILNGVPAQ 348
Qy 209 -----NYTCVVTYPENGRTFHLTRTLTKVVGSPKNAVPPVHSPNDHVYVEKEPGEEL 262
Db 349 PLGPRAQLLKATPEDNGRSFSCSATL--EVAGQ-----LIH-----KNQTRREL 390
Qy 263 LIPCTVYFSLMDSR-----NEVWMTIDGKKP-----DDITIDVTINESIS 303
Db 391 ----RVLYGPRLDERDCPGNWTWPENSQQTPMCQAWGNPLPELKLKDGTFPLPIGESVT 446
Qy 304 HSRTEDETRQILSIKKVTSSEDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVLACG 363
Db 447 VTR-----DLEGTYLCRARSTQGEVTR--EVTNVLSPRVEI----- 481
Qy 364 FGATVLLVILIVVYHYVWLEWLVFYR 390
Db 482 ---VIITVVAANVIMGTAGLSTYLYNR 505

RESULT 11
US-11-016-503-10
; Sequence 10, Application US/11016503
; Publication No. US2005024547A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-503-10

Query Match      2.9%; Score 106; DB 7; Length 567;
Best Local Similarity 19.6%; Pred. No. 0.069;
Matches 86; Conservative 49; Mismatches 132; Indels 172; Gaps 22;

Qy 87 LPENRISKEDVWLWFRPTLLNDTGNVTC--MLRNTTY-----CSKVAFPL-----EVV 132
Db 63 LPE-MVSKESERLSITKSACGRNGKQFCSTLTTLTAQANHGTGFSYCKYLAVPTSKKETE 121
Qy 133 QKDCSCNSPMKLPVHKLYIEY-----GIQ-----RITCPNVDGVSFSSVPTITWYM 179
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Qy 266 CTVYFSLMDSRNEVWWTIDGKKPDDITIDVTINESISHSRTEDETRTQILSIKKVTSE 325
Db 2368 C-----EAKGEMPKVTLWSP-----TNKVIPTSSKEYQIYQDGT-----LLIQAKRSD 2412
Qy 326 LKRSYVCHARSAGKAVAKAVKQV-----PAPRYTV-ELACGFGATVLLVWIL-- 374
Db 2413 -SGNYTCLVRNSAGEDRTVMHVNVPKPNPNPITTVRETAAG-GSKRLDCKAEG 2470
Qy 375 IWVHVYWL--EMVLFYRAHFGTDETDLDGKEYDIYVSYARNABEEFVLLTLRGLVLE 432
Db 2471 IPTPRVLWAFPEGVVLPAFYGNRITVHGNSLDI-----RSLAKSDSVQLVC--MARNE 2523
Qy 433 FGKLCIFDRSLPGNTVEAFDFIQSRMIV---VLSP-----DYVTEKSIWLE 482
Db 2524 GG-----EARLIQVLTVLEPMEKPIFHPDISEKITAMAG 2557
Qy 483 FKLGMVC 489
Db 2558 HTISLNC 2564
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## RESULT 14

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US-11-135-855-36
; Sequence 36, Application US/11135855.
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; PRIOR FILING DATE: 2005-05-24
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-36
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Query Match 2.9%; Score 105; DB 7; Length 1694;
Best Local Similarity 20.8%; Pred. No. 0.41; Mismatches 85; Indels 80; Gaps 13;
Matches 55; Conservative 44;

Qy 108 DTGNYTCMLR-----NTTYCSKVAFPLEVYVQKDCSFNSPMKLPVHKLYIEYGIQRTCP 161
Db 1229 DEGFYSCARSPLQANTSLELRLEGVRVILAPAAV--PEGAPI-----TVTCA 1276

Qy 162 NVDGYPSSVKPTI--TWYMCYKIQNNVPIEG--MNLISFLIALISNNGNYTCVWTYPE 218
Db 1277 D-----PAAHAPTLYTWYHNGRWLQ-----EGPAASLSFLVATRAHAGAYSQAOQDA 1324

Qy 219 NGRTFHLTRLTVKVGSPKNVPPVIHSPNDHVHYEKEPGEELLIPCTVYVFSFLMDSRN 278
Db 1325 GTR-----SSRPAALQVLYAPQDAVL-----SSFRDSRA 1353

Qy 279 E-----VWMTIDGKKPDDITID-----VTINESISHSRTEDETRTQI-----LSIKKVTSE 324
Db 1354 RSMAVIOCTVDSEPPAELASHDGKVLATSSGVHSLASGTGHVQVARNALRLQVDVPAG 1413

Qy 325 DLKRSYVCHARSAGKAVAKAVK 348
Db 1414 D--DTYVCTAQNLLGISISTIGRLQ 1435
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Search completed: December 7, 2005, 13:47:20  
Job time : 15 secs

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RESULT 15
US-11-135-855-35
; Sequence 35, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; PRIOR FILING DATE: 2005-05-24
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-35
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Query Match 2.9%; Score 105; DB 7; Length 1709;
Best Local Similarity 20.8%; Pred. No. 0.42; Mismatches 85; Indels 80; Gaps 13;
Matches 55; Conservative 44;

Qy 108 DTGNYTCMLR-----NTTYCSKVAFPLEVYVQKDCSFNSPMKLPVHKLYIEYGIQRTCP 161
Db 1229 DEGFYSCARSPLQANTSLELRLEGVRVILAPAAV--PEGAPI-----TVTCA 1276

Qy 162 NVDGYPSSVKPTI--TWYMCYKIQNNVPIEG--MNLISFLIALISNNGNYTCVWTYPE 218
Db 1277 D-----PAAHAPTLYTWYHNGRWLQ-----EGPAASLSFLVATRAHAGAYSQAOQDA 1324

Qy 219 NGRTFHLTRLTVKVGSPKNVPPVIHSPNDHVHYEKEPGEELLIPCTVYVFSFLMDSRN 278
Db 1325 GTR-----SSRPAALQVLYAPQDAVL-----SSFRDSRA 1353

Qy 279 E-----VWMTIDGKKPDDITID-----VTINESISHSRTEDETRTQI-----LSIKKVTSE 324
Db 1354 RSMAVIOCTVDSEPPAELASHDGKVLATSSGVHSLASGTGHVQVARNALRLQVDVPAG 1413

Qy 325 DLKRSYVCHARSAGKAVAKAVK 348
Db 1414 D--DTYVCTAQNLLGISISTIGRLQ 1435
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 14, 2005, 11:46:30 ; Search time 322 Seconds  
(without alignments)  
3792.500 Million cell updates/sec

Title: US-10-061-727-2  
Perfect score: 3669  
Sequence: 1 MTLMLCVSLVSYFYGIQSDA.....SALALHFTDLNNDFYIL 687

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO\_spool/US10061727/runat\_07122005\_113337\_17228/app\_query.fasta\_1.839  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2591.5	70.6	4724	3	US-09-949-016-313
2	2591.5	70.6	4726	3	US-09-949-016-5448
3	2586	70.5	1740	3	US-08-991-944-1
4	2327.5	63.4	3355	3	US-08-991-944-3
5	1938	52.8	2748	3	US-10-282-162-51
6	1937.5	52.8	2754	3	US-10-282-162-53
7	1937.5	52.8	2754	3	US-10-282-162-55
8	1935	52.7	2703	3	US-10-282-162-39
9	1935	52.7	2709	3	US-10-282-162-41

10	1935	52.7	2709	3	US-10-282-162-43	Sequence 43, Appl
11	1930	52.6	2733	3	US-09-313-942-27	Sequence 27, Appl
12	1930	52.6	2733	3	US-10-282-162-27	Sequence 27, Appl
13	1833	50.0	2703	3	US-10-282-162-33	Sequence 33, Appl
14	1833	50.0	2709	3	US-10-282-162-35	Sequence 35, Appl
15	1833	50.0	2709	3	US-10-282-162-37	Sequence 37, Appl
16	1830	49.9	2754	3	US-10-282-162-47	Sequence 47, Appl
17	1830	49.9	2754	3	US-10-282-162-49	Sequence 49, Appl
18	1829	49.9	2748	3	US-10-282-162-45	Sequence 45, Appl
19	825	22.5	2061	3	US-09-173-151A-3	Sequence 3, Appl
20	800	21.8	1737	3	US-09-173-151A-1	Sequence 1, Appl
21	767	20.9	2537	3	US-09-173-151A-34	Sequence 34, Appl
22	536	14.6	141454	3	US-09-949-016-12055	Sequence 12055, A
23	536	14.6	141455	3	US-09-949-016-17190	Sequence 17190, A
24	528.5	14.4	1620	3	US-08-996-338-7	Sequence 7, Appl
25	528.5	14.4	1620	2	US-09-556-972-7	Sequence 7, Appl
26	528	14.4	1626	2	US-08-604-333-1	Sequence 1, Appl
27	528	14.4	1626	3	US-09-110-618-1	Sequence 1, Appl
28	528	14.4	1626	3	US-09-578-178-1	Sequence 1, Appl
29	528	14.4	1626	3	US-09-577-806-1	Sequence 1, Appl
30	528	14.4	1626	3	US-09-621-502-3	Sequence 3, Appl
31	528	14.4	3522	3	US-09-023-655-906	Sequence 906, App
32	528	14.4	3522	3	US-09-949-002-74	Sequence 74, Appl
33	520	14.2	1563	3	US-09-949-002-203	Sequence 203, App
34	520	14.2	1563	3	US-08-996-338-1	Sequence 1, Appl
35	520	14.2	1563	3	US-09-556-972-1	Sequence 1, Appl
36	495	13.5	2314	3	US-09-173-151A-9	Sequence 9, Appl
37	495	13.5	2668	3	US-09-949-002-204	Sequence 204, App
38	495	13.5	2681	3	US-09-621-502-1	Sequence 1, Appl
39	495	13.5	2681	3	US-09-616-530A-6	Sequence 6, Appl
40	495	13.5	2681	3	US-10-212-356A-6	Sequence 6, Appl
41	495	13.5	2681	3	US-10-212-287-6	Sequence 6, Appl
42	495	13.5	2681	3	US-09-949-002-72	Sequence 72, Appl
43	488.5	13.3	2356	2	US-07-821-716-3	Sequence 3, Appl
44	484.5	13.2	1782	2	US-08-381-603-3	Sequence 3, Appl
45	484.5	13.2	1782	3	US-08-924-376-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-949-016-313  
; Sequence 313, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 313  
; LENGTH: 4724  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-313

Alignment Scores:  
Pred. No.: 1.16e-258 Length: 4724  
Score: 2591.50 Matches: 502  
Percent Similarity: 86.84% Conservative: 39  
Best Local Similarity: 80.58% Mismatches: 50  
Query Match: 70.63% Indels: 32  
DB: 3 Gaps: 7

US-10-061-727-2 (1-687) x US-09-949-016-313 (1-4724)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
Db 207 ATGACACTTCGTGGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 266  
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
Db 267 TCAGAACGCTCGGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 326  
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
Db 327 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAAACACTTCTTGAAATTCACACTACAGCACA 386  
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80  
Db 387 GCCCATTCAGTGGCCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGGAG 446  
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
Db 447 GAGCCAAATTAACTTCCCGCTCCCGAGAACCCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 506  
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
Db 507 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCGATGTTAAGGAACACTPACA 566  
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
Db 567 TATTGCAGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 626  
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
Db 627 CCCATGAACATCCAGTGCATAAATCTGTATAGAAATATGCAATTCAGAGGATCACTTGT 686  
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180  
Db 687 CCAAATGTAGATGATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGC 746  
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Db 747 TGTTATAAAATACAGAATTTTAAATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 806  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
Db 807 ATTCCCTTAAATTTCAAAATAATGGAATTTACACATGTGTGTGTATACATATCCAGAAAATGGA 866  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Db 867 CGTACGTTTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATAATGCA 926  
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
Db 927 GTGCCCCCTGTGATCCATTCACCTTAATGATCATGTGTCTATGAGAAAGAACCAGGAGAG 986  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
Db 987 GAGCTACTCATTCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTCGCAATGAGGTT 1046  
Qy 281 TrpTrpThrIleAspGlyLysLeuProAspAspIleThrIleAspValThrIleAsnGlu 300  
Db 1047 TGGTGGACCAATTGATGAAAATAAACCTGATGACATCACTATTGATGTCACCAATTAAACGAA 1106  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
Db 1107 AGTATAAGTCATAGTACAGAGAAGATGAACCAAGAACTCAGATTTTGACCATCAAGAAA 1166  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
Db 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTATGCTAGAGTGCACAAAGCGAA 1226  
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
Db 1227 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGGCCAGCTCCAGATACACAGTGGAACTG 1286

Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValIleLeuIleValValTyrHisVal 380  
Db 1287 GCTTGTGGTTTTGGAGCCACAGCTCCTGCTAGTGGTGATTCTCATTTGTGTATTACCATGTT 1346  
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400  
Db 1347 TACTGGCTAGAGATGGTCTTATTTACCGGGCTCATTTTGGAAACAGATGAACCATTTTA 1406  
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluGluPhe 420  
Db 1407 GATGGAAGAAGATGATGATATTTATGATCTCTATGCAAGGAATGCGGAAGAAGAATTT 1466  
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440  
Db 1467 GTATTACTGACCCCTCCGTGGAGTTTGGAGAATGAATTTGGATACAAAGCTGTGCATCTTT 1526  
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460  
Db 1527 GACCGAGACAGTCTGCTCGGGGAATTTGTCCACAGATGAGACTTTGAGCTTCATTTCAGAA 1586  
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480  
Db 1587 AGCAGACGCTCTCTGGTGTCTTAAGCCCACTACGTGCTCCAGGGAACCCAGGCCTC 1646  
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496  
Db 1647 CTGGAGCTCAAGGCTGGCCTA-----GAAATATATGGCTCTCTCGGGCAACATCAAC 1697  
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516  
Db 1698 GTCATTTTAGTACAGTACAAAGCTGTGAAGGAACACGAAG-----GTGAAGAGCTGAAG 1751  
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyLysSerLysHisSerGly 533  
Db 1752 AGGCTTAAGACGCTGCTCAGGTCATTAAATGGAAGGGGAAATAATCCAGTATCCACAG 1811  
Qy 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553  
Db 1812 GGCAGGTTCTGGAAGCAGCTGCAGGTGGCCATCCAGTGAAGAAAGTCCCAGCGGTCT 1871  
Qy 554 GlyTrpAsnGlnSerCysSerSerGlnSerAspIleSerLeuAspHisVal-GlnArgAr 573  
Db 1872 AGCAGTGTAGCAGGCGCTCTCGTATTCA-----TCTTTGAAAAATGTATGAAGGAA 1925  
Qy 573 GArg-----SerArgLeuLysGluProProGluLeuG1 584  
Db 1926 TAATGAAAGGTTAAAGNACAAAGGGTCTCCAGGAAGAAAGATGCCCCAG----- 1980  
Qy 584 nSerSerGluArgAlaGlySerProAlaProGly\*\*\*MetSerLysHisArgG1 604  
Db 1981 -----TCTTTCATTGCGAGTTTATGTTTCATAGGCAAAAATAATGG 2021  
Qy 604 YLysSer 606  
Db 2022 TCTAAGC 2028

## RESULT 2

US-09-949-016-5448  
; Sequence 5448, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5448  
 ; LENGTH: 4726  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-5448

Alignment Scores:  
 Pred. No.: 1,16e-258 Length: 4726  
 Score: 2591.50 Matches: 502  
 Percent Similarity: 86.84% Conservative: 39  
 Best Local Similarity: 80.58% Mismatches: 50  
 Query Match: 70.63% Indels: 32  
 DB: 3 Gaps: 7

US-10-061-727-2 (1-687) x US-09-949-016-5448 (1-4726)

QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
 DB 207 ATGACATTCCTGGTGTGTAGTCTCTACTTTTATGGAACTCTGCNAAGTGTATGCC 266  
 QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
 DB 267 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTTCAGAT 326  
 QY 41 GluProAlaArgIleIleCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
 DB 327 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACACTCTTGTGAATTCAACTACACACA 386  
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80  
 DB 387 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTGGACTAGCACGACCGGGACCTTGAG 446  
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
 DB 447 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGG 506  
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
 DB 507 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCACTGTTAAGGAACACTACA 566  
 QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
 DB 567 TATTGCAGCAAGTTGCAATTCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 626  
 QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
 DB 627 CCCATGAACCTCCAGTGCATAAATCTGTATAGAAATATGGCAATTCAGAGGATCACTTGT 686  
 QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180  
 DB 687 CAAATGTAGATGGATATTTTCCATGTCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 746  
 QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
 DB 747 TGTATAAATACAGAAATTTAATATGTAATACCCGAGAGGTATGAACTTGAGTTTCCTC 806  
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
 DB 807 ATTGCTTAATTTCAAAATAATGGAATTTACACATGTGTGTTGTACATATCCAGAAAATGGA 866  
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
 DB 867 CGTAGTTTCACTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATAATGCA 926  
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
 DB 927 GTGCCCTCTGTATGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 986  
 QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280

DB 987 GAGCTACTCATTCCTCGTACGGTCTATTTTAGTTTTCGTAGTATTCGCAATGAGGTT 1046  
 QY 281 TrpTrpThrIleAspGlyLysProAspAspIleThrIleAspValThrIleAsnGlu 300  
 DB 1047 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTATGATGTCCACATTAACGAA 1106  
 QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
 DB 1107 AGTATAAGTCATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1166  
 QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
 DB 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGCTAGTGTGATTTCTCATTTGTTTACCATGTT 1226  
 QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
 DB 1227 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGAACATG 1286  
 QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380  
 DB 1287 GCTTGTGGTTTGGAGCCACAGTCTCTGCTAGTGGTGAATTTCTCATTTGTTTACCATGTT 1346  
 QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400  
 DB 1347 TACTGGCTAGAGATGCTCTATTTTACCGGGCTCATTTTGGAAACAGATGAACCATTTTA 1406  
 QY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420  
 DB 1407 GATGAAAGAGTATGATATTTATGTATCTTATGCAAGAAATGCGGAAGAAAGAAATTT 1466  
 QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440  
 DB 1467 GTATTACTGACCTCCGTTGGAGTGTGGAGAAATGNAATTTGGATACAAAGCTGTGCATCTTT 1526  
 QY 441 AspArgAspSerLeuProGlyLysAsnThrValGluAlaValPheAspPheIleGlnArg 460  
 DB 1527 GACCGAGACAGCTGCTCGCTGGGGAAATGTACAGATGAGACTTTGAGCTTCATTTCAGAAA 1586  
 QY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480  
 DB 1587 AGCAGACGCTCTCGTGTGTTTCTAAGCCCCAACCTACGTGCTCCAGGGAAACCCAGCCCTC 1646  
 QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys 496  
 DB 1647 CTGGAGCTCAAGCTGGGCTA-----GAAATATGGCTCTCGGGGCAACATCAAC 1697  
 QY 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516  
 DB 1698 GTCATTTTAGTACAGTACAAAGCTGTGAAGGAAACGAAAG-----GTGAAGAGAGCTGAAG 1751  
 QY 517 GluSer-----ValSerPheValSerTrpLysGlyLysSerLysHisSerGly 533  
 DB 1752 AGGCTTAAGACGGTCTCACGGTCAATTAATGGAAGGGGAAAAATCCCAAGTATCCACAG 1811  
 QY 534 SerLysPheTyrLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553  
 DB 1812 GGCAGGTTCTGGAAGCAGCTGCGAGTGGCCATGCGAGTGAAGAAAGTCCCGCCGGCTCT 1871  
 QY 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisVal-GlnArg 573  
 DB 1872 AGCAGTGTAGCAGGGGCTCTCGTATTCA-----TCTTTGAAAAATGTATGAAAGGAA 1925  
 QY 573 gArg-----SerArgLeuLysGluProProGluLeuGlu 584  
 DB 1926 TAATGAAAGGGTAAAAAGAACAAAGGGGTGCTCCAGGAAGAAAGAGTCCCGCCAG- 1980  
 QY 584 nSerSerGluArgAlaAlaGlySerProProAlaProGly\*\*MetSerLysHisArgGlu 604  
 DB 1981 -----TCTTCATTCGCGAGTTTATGTTTTCATAGCAAAAAAATATGCG 2021  
 QY 604 yLysSer 606  
 DB 2022 TCTAAGC 2028

## RESULT 3

US-08-991-944-1  
; Sequence 1, Application US/08991944  
; Patent No. 6280955  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Zhaodan  
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,  
; Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94010  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,944  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 343-4341  
; TELEFAX: (650) 343-4342  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1740 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 10...1719  
US-08-991-944-1

## Alignment Scores:

Pred. No.:	7,57e-259	Length:	1740
Score:	2586.00	Matches:	488
Percent Similarity:	91.43%	Conservative:	35
Best Local Similarity:	85.31%	Mismatches:	37
Query Match:	70.48%	Indels:	12
DB:	3	Gaps:	4

US-10-061-727-2 (1-687) x US-08-991-944-1 (1-1740)

Qy	1	MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla	20
Db	10	ATGACACTTCTGTGGTGTAGTGAGTCTTACTTTTATGGAAATCCTGCAAGGTGATGCC	69
Qy	21	SerGluArgCysAspAsnTrpGlyLeuAspTrpMetArgGlnIleGlnValPheGluAsp	40
Db	70	TCAGAACGCTCGGATGACTGGGGACTAGACACCATGAGGCAATCCCAAGTGTTTGAAGAT	129
Qy	41	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	60
Db	130	GAGCCAGCTCGCATCAAGTGCCTACTCTTTGAACACTCTTTGAAATTCACACTACAGACA	189
Qy	61	AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu	80
Db	190	GCCCATTCAGCTGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG	249
Qy	81	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp	100

Db	250	GAGCCAATTAACTTCCGCCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGCTGCTGG	309
Qy	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	120
Db	310	TTCCGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGTCATGTTTAAGGAACACTACA	369
Qy	121	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	140
Db	370	TATTGCAGCAAAAGTTGCAATTTCCCTTGGAAAGTTTCCAAAAAGACAGCTGTTTCAATTCC	429
Qy	141	ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys	160
Db	430	CCCATGAACCTCCAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGATCATTGT	489
Qy	161	ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly	180
Db	490	CCAAATGTAGATGGATATTTTCTTCCAGTGTCAACCGACTATCACTTGGTATATGGGC	549
Qy	181	CysTyrLysIleGlnAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu	200
Db	550	TGTTATAAAATACAGAAATTTTAATATGTAATACCCGAAGGTATGAACTTGAGTTTCCCTC	609
Qy	201	IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly	220
Db	610	ATTGCCCTTAATTTCAAATAATATGGAATACATGTGTTGTACATATCCAGAAATGGA	669
Qy	221	ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	240
Db	670	CGTACGTTTTCATCTCACCGAGCTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA	729
Qy	241	ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	260
Db	730	GTGCCCCCTGTGATCCATTCCACTAATGATCATGTGCTCTATGAGAAAGAACCAAGGAG	789
Qy	261	GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	280
Db	790	GAGCTACTCAITTCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT	849
Qy	281	TrpTrpThrIleAspGlyLysLysProAspAspileThrIleAspValThrIleAsnGlu	300
Db	850	TGGTGGACCATTTGATGAAAAAACCCTGATGACATCACTATTGATGTCACTTAACGAA	909
Qy	301	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	320
Db	910	AGTATAGTCAATAGTAGAAGAGATGAAACAAAGAACTCAGATTTTGGAGCATCAAGAA	969
Qy	321	ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	340
Db	970	GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTCATGCTAGAGTGCACAAAGGCGAA	1029
Qy	341	ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu	360
Db	1030	GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTG	1089
Qy	361	AlaCysGlyPheGlyAlaThrValLeuLeuValIleLeuIleValValTyrHisVal	380
Db	1090	GCTTGTGTTTGGAGCCACAGCTCTGTAGTGTGATTCTCATTTGTTTACCATGTT	1149
Qy	381	TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu	400
Db	1150	TACTGGCTAGAGATGGTCTTATTTTACCGGGCTCATTTTGGACACAGATGAACCATTTTA	1209
Qy	401	AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe	420
Db	1210	GATGGAAAAAGAGTATGATATTTATGATCTCTATGCAAGGAATGCGGAAGAAAGAAATTT	1269
Qy	421	ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe	440
Db	1270	GTATTACTGACCTCCGTGGAGTTTGGAGAAATGAAATTTGGATACAAAGCTGTGATCTTT	1329
Qy	441	AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg	460
Db	1330	GACCGAGACAGTCTGCTCGGGGAATTTGTACAGATGAGACTTTGAGCTTCATTTCAGAA	1389

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QY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
DB 1390 AGCAGAGCGCTCTCTGGTGTCTTAAAGCCCACTAGTGTCTCCAGGGAACCCCAAGCCCTC 1449
QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys-----496
DB 1450 CTGGAGCTCAAGGCTGCCTA-----GAAATATGSCCTCTCGGGGCAACATCAAC 1500
QY 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
DB 1501 GTCATTTTAGTACAGTACAAAGCTGTGAAGAAACGAAG-----GTGAAAGAGCTGAAG 1554
QY 517 GluSer-----ValSerPheValSerTrpLysGlyLysLysSerLysHisSerGly 533
DB 1555 AGGCTAAGACGGTGTCTCAGCGTCATTAAATGAAGAGGGGAAATCAAGTATCCACAG 1614
QY 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
DB 1615 GGCAGGTTCTGGAAGCAGCTGCAGGTGGCCATGCCAGTGAAGAAAGTCCAGGCGGTCT 1674
QY 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIle 565
DB 1675 AGCAGTGATGAGCAGCGGCTCTCGTATTCTATTCTTTG 1710
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## RESULT 4

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US-08-991-944-3
; Sequence 3, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaoan
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
; TITLE OF INVENTION: Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/991,944
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..1844
US-08-991-944-3
Alignment Scores:
Pred. No.: 2,046-231
Score: 2327.50
Percent Similarity: 83.36%
Length: 3355
Matches: 443
Conservative: 73
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Best Local Similarity: 71.57% Mismatches: 76
Query Match: 63.44% Indels: 28
DB: 3 Gaps: 8
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US-10-061-727-2 (1-687) x US-08-991-944-3 (1-3355)

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QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
DB 135 ATGGACCTCTCTGGTATTGATAGTCTGTCTTCTATGGGATCTTCGAGAGTCTATGCT 194
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 195 TCGGAGCGCTGTGATGACTGGGGACTAGATACCATCGGACAAATCCAAAGTGTTCGAAGAT 254
QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 255 GAGCGCGCTCGAATCAAGTGGCCCTCTTTGAACACTTCTCCTGAAGTACAACTACAGCACT 314
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 315 GCCCATTTCTCTGGGCTTACCTGATCTGGTACTGGACCAAGAACCCGGGACCTGGAG 374
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
DB 375 GAGCCCATTAACCTTCGGCTCCACAGAAATCGCATCAGTAAGGAGAAAGATGTGCTCTGG 434
QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 435 TTCCGGCCACCCCTCTCAATGACACGGGCAATTACACCTGCATGTGTGAGGAACAACACT 494
QY 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
DB 495 TACTGCAGCAAGTTGCAATTTCCCTGGAAGTTGTTTCAAGAGGACAGCTGTTTCAATTC 554
QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 555 GCCATGAGATTCCCGAGTGCACAGATGTATATTGAACATGGCATTCATAAGATCACATGT 614
QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
DB 615 CCAAAATGTAGACGGATACTTTCTTCCAGTGTCAAAACCATCGGTCTATGAGGTATAGG 674
QY 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 675 TGTAAGTAAATAGTGGACTTTTCAATAATGTATTACCCGAGGGGATGAATCTGAGCTTTTC 734
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
DB 735 ATCCCTTGGTTTCAATAACGGAAATTTACACATGTGTGGTTTACATATCTCTGAAACCGA 794
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
DB 795 CGTCTCTTTCACTCACCGAGCTGTGACTGTAAAGGTGGTGGGCTCACCAAAAGGATGCA 854
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB 855 TTGCCACCCAGATCTATTCTTCCAAATGACCGTGTGTGTATGAGAAAGAACCCAGAGAG 914
QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
DB 915 GAACTGGTTATTCCTCGCAAGTCTATTTCAGTTTTCATTATGGACTCCCAACATGAGGTC 974
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB 975 TGGTGGACCATTTGATGGAAGAAGCCGTGATGACGTGCACAGTCACATCTATTAAATGAA 1034
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 1035 AGTGAAGTATTCTTCAACGGAAAGATGAAACAAAGGACTTCAGATTTTGGAGCATCAAGAA 1094
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
DB 1095 GTACCCCGGAGGATCTCAGGCGCAACTATGTCTGTCTATGCTCGAATATACCAAGGGGNA 1154
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QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1155 GCTGAGCAGGCTGCCAAGGTGAAACAGAAAGTATACACCAAGGTACACAGTAGAAGTCTC 1214
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValLysLeuValLysValValTyrHisVal 380
Db 1215 GCCTGTGGTTTGGAGCCACGGTCTTCTGTGTAGTGGTCTCATTTGGTTTACCATGTT 1274
QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1275 TACTGGCTGGAGATGGTCTCTTTTACCGAGCTCACCTTTGGAAACAGATGAACAATCTT 1334
QY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db 1335 GATGGAAGGAGTATGATATTTATGTTTCTTATCAAGAAATGTGGAAGAGAGGAATTT 1394
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1395 GTGCTGTGACGCTGCGTGGAGTTTGGAGNAATGAGTTTGGATACAAAGCTGTGCAATCTTC 1454
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1455 GACAGACAGACCCCTGCGGGAATTTGTACAGATGAGACCCCTGAGCTTCATTCAGAAA 1514
QY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1515 AGCAGACAGCTCCCTGGTGTCTTAAGTCCCAACTACGTGTCCAGGAACAACAAGCCCTC 1574
QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
Db 1575 CTGGAGCTCAAGGCTGGCCTA-----GAAATATAGCCTCCCGGGGCAACATCAAC 1625
QY 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLys 516
Db 1626 GTCAATTTAGTGCAAGTACAAAGCTGTGAAGACATGAAG-----GTGAAAGAGCTGAAG 1679
QY 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1680 CGGCTGAAGCAGGTGCTCAAGTCAATTAATGGAAGGAGAGAAATCCAAGTATCCTCAG 1739
QY 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1740 GGCAGGTTCTGGAAGCAGTTGCAGGTGCCATGCCAGTGAAGAG-----AGTCCC 1790
QY 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArg 573
Db 1791 AGTGGTCT-----AGCAATGACAAGCAGGG-TCTCTCTACTCATCCCTGMAAAA 1840
QY 574 ArgSerArgLeuLysGluProGluLeuGlnSerSerGluArgAlaAlaGlySer--- 592
Db 1841 CGTATGAAA-----GGAAAGTGAGGGGGGTACAAAGAACACGCGGTTCATGG 1888
QY 593 -----ProProAla-ProGly***MetSerLysHisArgGlyLysSerSer 607
Db 1889 GAGGAAGGGCCCTCTTTCTCTTAGGCTGTGGCTTCATAGACAGAAAAGAGT 1943

RESULT 5
US-10-282-162-51
; Sequence 51, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
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; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 51  
; LENGTH: 2748  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-282-162-51

Alignment Scores: 5.47e-191 Length: 2748  
Pred. No.: 1938.00 Matches: 432  
Score: 63.42% Conservat: 50  
Best Local Similarity: 56.84% Mismatches: 141  
Query Match: 52.82% Indels: 140  
DB: 3 Gaps: 19

US-10-061-727-2 (1-687) x US-10-282-162-51 (1-2748)

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QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGGCTTCTGTGGTGTGTAGTGTCTCTCTTTTATGGAATCTCTGCAAAAGTATGCC 60
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120
QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCACCTCTTTTGAACACTTCTTGAATTTCAACTACAGACA 180
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCATTACGCTGGCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 240
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATAACTTCCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG 300
QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCTCAATGACACTGCACTATACCTGTCATGTGTTAAGGAAACATACA 360
QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATCC 420
QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCAGTGTCATAAACTGTATATAGAAATATGGCATTTCAGAGGATCCTTGT 480
QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAAAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTTATAAATAACAGAAATTTTAAATAATGTAATACCCGGAAGGTATGAATCTTGAGTTTCTC 600
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCCTTAATTTCAAAATAAATAAATTAACACATGTGTGTATACATATCCAGAAAAATGGA 660
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACCTTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATTCCTTGTAGCGGTCTATTTTAGTTTCTGATGATGATCTTCGCAATGAGGTT 840
```



Qy	281	TrpTrpThrIleAspGlyLysLeuPheProAspAspIleThrIleAspValThrIleAsnGlu	300
Db	841	TGGTGGACCATTTGATGAAAAAACCTGATGACATCACTATTGATGTGCACATTAACGAA	900
Qy	301	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	320
Db	901	AGTATAGTTCATGTAGAACAGAAGATGAACAAGAAGAACTCAGATTTTGGAGCATCAAGAA	960
Qy	321	ValThrSerGluAspLeuLysAspSerTyrValCysHisAlaArgSerAlaLysGlyGlu	340
Db	961	GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTCATGTAGAAGTGCCAAAGCGCAA	1020
Qy	341	ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu	360
Db	1021	GTTGCCAAGCAGCAAGGTGAAGCAAGATGCGAGTCCAGATACACAGTGCACACA	1080
Qy	361	-----AlaCysGlyPhe-----	364
Db	1081	GGGGCTGCCAAGAGCTCCGGTTTCGTGGAGGAGCATTAAGCGGGAGTTCAAGCTGGAA	1140
Qy	365	GlyAlaThrValLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu	384
Db	1141	GGGGAGCTGTAGCCCTGAGGTGCCCCAGGTG-----CCCTACTGGTTGTGG	1188
Qy	385	MetValLeuPheTyrArgAlaHisPhe-----	393
Db	1189	GCCTCTGTGAGCCCCGCATCAACCTGCATGGCATAAATAAGTACTCTGTAGGACGGTC	1248
Qy	394	--GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla	412
Db	1249	CCAGGAAGAAGACAGACAGCATGTGGGCCAGGACGGTGCTCTGTGGCTTCTGCCAGCC	1308
Qy	413	ArgAsnAlaGluGluGluPuPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu	432
Db	1309	TTGCAGAGAGACTCTGSCACTAGCTCTGCACACTACTAGAAATGCTCTTACTGTGACAA	1368
Qy	433	PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu	452
Db	1369	ATGTCCATTGAGCTCAGAGTTTTTGAG-----AATACA---GAT	1404
Qy	453	AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal	467
Db	1405	GCCTTCTCGGTTCATCTCATACCCGCAATTTTAACTTGTCAACCTCTGGGGTATTA	1464
Qy	468	LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal	487
Db	1465	GTATGCCCTGAC-----CTGAGTGAATTC-----	1488
Qy	488	MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis	507
Db	1489	-----ACCCGTGACAAACTGACGTGAAGATTCAATGGTACAAG-----	1527
Qy	508	ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu	527
Db	1528	-----GATTTCTCTCTTTTGGATAAAGACAATGAGAGAAATTTCTAAGTGTGAGGGGACC	1581
Qy	528	LysSer-----	529
Db	1582	ACTCACTTACTGTACAGATGTGGCCCTGGAAGATGCTGCTATTACCCTGTGTCCTG	1641
Qy	530	-----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu---	544
Db	1642	ACATTTGCCCATGAAGGCCAGCAATACACATCATCTAGGAGTATTGAGCTACGCATCAAG	1701
Qy	545	-----ProLeuArgSerLeuSerAlaSer	552
Db	1702	AAAAAAAAAAGAGACACATTCTCTGTGATCATTTTCCCGCTCAAGACCATATCAGCTTCT	1761
Qy	553	SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg	572
Db	1762	CTGGGG-----TCAAG-AC TGACAACTCCCAATGAAGTGTTTCTGGG	1802
Qy	573	ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu	587

```

Db      1803 AACCGGCACACCCCTTAAACCAACCACCTGCTGTGGTGGACGGCCAAATGACACACCCACATAGAGAG 1862
      |||
      :
      :
      :
Qy      588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
      |||
      :
      :
      :
Db      1863 CGCTACCGGGAGGCGCGTGACCGGAGGGGCCACGCCAGGAATATTTCAGAAATAATGA 1922
      |||
      :
      :
      :
Qy      602 -----HisArgGlyLysSerSerAla 608
      :
      :
      :
      :
Db      1923 GAACTACATTGAAGTGCATTTGATTTTGTCTGTGTCAAGAGAGGATTTGCACATGGA 1982
      |||
      :
      :
      :
Qy      609 ThrCysArgCysCysValThrTyrcysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
      |||
      :
      :
      :
Db      1983 TTTTAAATGTGTTGCTCCATAATACCCCTGAGTT-TCAGACACTACGCACACCACTCAAGG 2041
      |||
      :
      :
      :
Qy      629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
      |||
      :
      :
      :
Db      2042 AAGCTCTCTCCAGTTCTCCGGAGAC-AAAACTCACACATGCCACCGTCCCGACGACCT 2100
      |||
      :
      :
      :
Qy      649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666
      |||
      :
      :
      :
Db      2101 GAA-----CTCCTGGGGGAGCGCTCAGTCTCTCTTCCCCCAAAACCCCAAG 2148
      |||
      :
      :
      :
RESULT 6
US-10-282-162-53
; Sequence 53, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-53

Alignment Scores:
Pred. No.: 6,19e-191 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
Db: 3 Gaps: 20

US-10-061-727-2 (1-687) x US-10-282-162-53 (1-2754)

Qy      1 MetThrLeuLeuTrpCysValSerValSerLeuTyrcysGlyLeuGlnSerAspAla 20
      |||
      :
      :
      :
Db      1 ATGGTGCTCTGTGGTGAGTGAGTCTCTACTTTATGGAATCTCTGCAAAAGTGATGCC 60
      |||
      :
      :
      :
Qy      21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
      |||
      :
      :
      :
Db      61 TCAGAACGCTGCATGATGCTGGGACATAGACACCATGAGGCAATCCCAAGTGTGTTGAAGAT 120
      |||
      :
      :
      :
Qy      41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrcysThr 60
      |||
      :
      :
      :
Db      121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAAACACTCTTTGAAATTTCAACTACAGCACA 180
      |||
      :
      :
      :
Qy      61 AlaHisSerAlaGlyLeuThrIleLeuTrpTyrcysGlnAspArgAspLeuGlu 80
      |||
      :
      :
      :
Db      181 GCCCATTCAGCTGCCCTTACTCTGATCTGGTATGGCATTAGGCAGGACCGGGACCTTGAG 240
      |||
      :
      :
      :
Qy      81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
      |||
      :
      :
      :

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! TITLE OF INVENTION: AND USING  
! FILE REFERENCE: REG 203-B-US  
! CURRENT APPLICATION NUMBER: US/10/282,162  
! CURRENT FILING DATE: 2002-10-28  
! PRIOR APPLICATION NUMBER: 09/787,835  
! PRIOR FILING DATE: 1999-09-22  
! PRIOR APPLICATION NUMBER: PCT/US99/22045  
! PRIOR FILING DATE: 1999-09-22  
! NUMBER OF SEQ ID NOS: 56  
! SOFTWARE: FastSeq for Windows Version 3.0  
! SEQ ID NO 55  
! LENGTH: 2754  
! TYPE: DNA  
! ORGANISM: Homo sapiens  
US-10-282-162-55

## Alignment Scores:

Pred. No.: 6,19e-191 Length: 2754  
Score: 1937.50 Matches: 432  
Percent Similarity: 62.06% Conservative: 49  
Best Local Similarity: 55.74% Mismatches: 135  
Query Match: 52.81% Indels: 161  
DB: 3 Gaps: 20

US-10-061-727-2 (1-687) x US-10-282-162-55 (1-2754)

```
QY 1 MetThrLeuLeuTyrCysValValSerLeuTyrPheTyrGlyLeuGlnSerAspAla 20
DB 1 ATGGTGCTTCTGTGTGTGTAGTAGTCTCTACTTTTATGGAATCCTGCAAGTAGATGCC 60

QY 21 SerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTTCAGAT 120

QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTGAATAATCAACTACAGCACA 180

QY 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCAATTGAGCTGGGCTTACTCTGATCTGTATGAGTAGGACGAGCGGACCTTGAG 240

QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGlyLysAspValLeuTyr 100
DB 241 GAGCCAAATTAATCTCCGCTCTCCCGAGAACCGCATTAGTAGGAGAAAGATGTGCTGTGG 300

QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 301 TTCCGGCCCACTCTCCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACAACACTACA 360

QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
DB 361 TATTGACGAAAGTGTGCAATTTCCCTTTGGAAGTGTTCAAAAGAGACAGCTGTTTCAATTC 420

QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 421 CCCATGAAATCCCAAGTCATAAATCTGTATATAGATATGGCAATTCAGAGGATCACTTGT 480

QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrPheMetGly 180
DB 481 CCAAAATAGATGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540

QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 541 TGTATATAAAATACAGAAATTTTAAATATGTAATACCCGGAAGGTATGAATCTGAGTTTCTC 600

QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
DB 601 ATTGCTTAAATTTCAAAATAATGGAATTTACACATGTGTGTGTATATCCAGAAAATGGA 660

QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
DB 661 CGTAGCTTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATAATGCA 720
```

```
QY 241 ValProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACAGAGAG 780

QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
DB 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGTAGTATTCGCAATGAGGTT 840

QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB 841 TGGTGGACCATGTGTAAGAAAACCTCATGACATCACTATTATGATGTCAACATTAACGAA 900

QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 901 AGTATAGTCATAGTAGAACAGAGAGTGAACAGACTCAGATTTTGAGCATCAAGAAA 960

QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
DB 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAGTGCACAAAGCGAA 1020

QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
DB 1021 GTTCCAAAGCAGCCAGGTGAAGCAGAAAGTGCAGCTCCAAGATACACAGTGCACACA 1080

QY 361 -----AlaCysGlyPhe----- 364
DB 1081 GGGGCTGCCAAGCTGCCGTTTCGTGGGAGGCATTAACAAGCGGAGTTCAGGCTGGAA 1140

QY 365 GlyAlaThrValLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
DB 1141 GGGGAGCCTGTAGCCCTGAGCTGCCCGCCAGGTG-----CCCTACTGTTGTTGG 1188

QY 385 MetValLeuPheTyrArgAlaHisPhe----- 393
DB 1189 GCCTCTGTGACCCCGCCGATCAACCTGACATGCGCATAAATAATGACTCTGTAGGACGGTC 1248

QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
DB 1249 CCAGAGAGAGAGACACCGATGTGGCCCGAGGACGGTCTGTGTGGCTCTGCGCAGCC 1308

QY 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
DB 1309 TTGCAGGAGGACTCTGGCACCTCGTCTGCACACTAGAGAAATGCTTCTTACTGTGACAAA 1368

QY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
DB 1369 ATGTCCCATTTGAGCTCAGAGTTTTTGG-----AATACA---GAT 1404

QY 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
DB 1405 GCTTTCCTGCGGTTCACTCATACCCGCAATTTTAACTTGTCAACCTCTGGGGTATTA 1464

QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
DB 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488

QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
DB 1489 -----ACCCGTCGAAAACTCAGCTGAAGATTTCAATGGTACAAAG----- 1527

QY 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
DB 1528 -----GATTCCTCTTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581

QY 528 LysSer----- 529
DB 1582 ACTCACTTACTCGTACAGCATGTGCCCTCGAAGATGCTGGCTATTATCCGCTGTGCTCGT 1641

QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
DB 1642 ACATTTGCCATGAAGCCAGCAATACAACTACTAGGAGTATTGAGCTACGCATCAAG 1701
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```
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-41

Alignment Scores:
Pred. No.:      1,1e-190      Length:      2709
Score:          1935.00      Matches:      358
Percent Similarity: 99.72%      Conservative: 0
Best Local Similarity: 99.72%      Mismatches: 1
Query Match:     52.74%      Indels:      0
DB:              3          Gaps:          0

US-10-061-727-2 (1-687) x US-10-282-162-41 (1-2709)

QY 1 MetThrLeuLeuTrpCysValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
DB 1 ATGGTGCTTCTGTGTGTAGTACTCTACCTTTTATGGAATCCTGCAAGTATGCC 60

QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTGGGAGTACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTGTTGAAGAT 120

QY 41 GluProAlaArgIleLeuLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTGAATTTCAACTACAGCACA 180

QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCATTCAGCTGGCTTACTCTGATCTGTATTTGGACTAGGACGAGCGGACCTTGAG 240

QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
DB 241 GAGCCAAATTAATCTCCGCTCTCCCGAGAACCCGATAGTAAGGAGAAAGATGTGCTGTGG 300

QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 301 TTCCGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAGGNACACTACA 360

QY 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
DB 361 TATTGACGAAAGTGTGCAATTTCCCTTGGAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420

QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 421 CCCATGAACATCCCACTAGTCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGT 480

QY 161 ProAsnValAspGlyTyrPheProSerValLysProThrIleThrTrpTyrMetGly 180
DB 481 CCANATGTAGATGGATATTTCTTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 540

QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 541 TGTATATAAATACAGAAATTTAATAATATGTAATACCCGAGGATGTAACCTTGAGTTTCCTC 600

QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
DB 601 ATTGCTTAAATTTCAAAATTAATGGAATTTACACATGTGTTGTATATATCCAGAAAATGGA 660

QY 221 ArgThrPheHisGluThrArgThrLeuThrValLysValIleGlySerProLysAsnAla 240
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```
DB 661 CGTAGCTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720

QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB 721 GTGCCCCCTGTGTATCCATTACCTAATGATCATGTGGTCTATGAGAAAAGAACCCAGGAG 780

QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
DB 781 GAGTACTCATCTCCCTGTACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGGTT 840

QY 281 TrpTrpThrIleAspGlyLysPheProAspPheThrIleAspValThrIleAsnGlu 300
DB 841 TGGTGGACCAATTGATGGAAAAAACCTGATGACATCACTATTGATGTCCCATTAACGAA 900

QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 901 AGTATAAGTCTATAGTAGAACAGAGATGAAACAAGAACTTCAGATTTTCAGCATCAAGAAA 960

QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
DB 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCTAGTAGAGTGCCAAAGCGGAA 1020

QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
DB 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGAA 1077

RESULT 10
US-10-282-162-43
; Sequence 43, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-43

Alignment Scores:
Pred. No.:      1,1e-190      Length:      2709
Score:          1935.00      Matches:      358
Percent Similarity: 99.72%      Conservative: 0
Best Local Similarity: 99.72%      Mismatches: 1
Query Match:     52.74%      Indels:      0
DB:              3          Gaps:          0

US-10-061-727-2 (1-687) x US-10-282-162-43 (1-2709)

QY 1 MetThrLeuLeuTrpCysValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
DB 1 ATGGTGCTTCTGTGTGTAGTACTCTACCTTTTATGGAATCCTGCAAGTATGCC 60

QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTCGCATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTGTTGAAGAT 120

QY 41 GluProAlaArgIleLeuLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTGAATTTCAACTACAGCACA 180

QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCATTCAGCTGGCTTACTCTGATCTGTATTTGGACTAGGACGAGCGGACCTTGAG 240

QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
DB 241 GAGCCAAATTAATCTCCGCTCTCCCGAGAACCCGATAGTAAGGAGAAAGATGTGCTGTGG 300

QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 301 TTCCGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAGGNACACTACA 360

QY 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
DB 361 TATTGACGAAAGTGTGCAATTTCCCTTGGAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420

QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 421 CCCATGAACATCCCACTAGTCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGT 480

QY 161 ProAsnValAspGlyTyrPheProSerValLysProThrIleThrTrpTyrMetGly 180
DB 481 CCANATGTAGATGGATATTTCTTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 540

QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 541 TGTATATAAATACAGAAATTTAATAATATGTAATACCCGAGGATGTAACCTTGAGTTTCCTC 600

QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
DB 601 ATTGCTTAAATTTCAAAATTAATGGAATTTACACATGTGTTGTATATATCCAGAAAATGGA 660

QY 221 ArgThrPheHisGluThrArgThrLeuThrValLysValIleGlySerProLysAsnAla 240
```

```
Db 181 GCCATTGAGTGGCTTACTCTGATCTGGTATTGGACTAGGACGAGCCGGACCTTGAG 240
Qy 81 GluProIleAenPheArgLeuProGluAenArgIleSerLysGluLysAenValLeuTrp 100
Db 241 GAGCAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGAGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAenAenPheThrGlyAenTyrThrCysMetLeuArgAenThrThr 120
Db 301 TTCCGGCCCACTCTCCCTCAATGACACTGGCAACTATATACCTGCGATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAenSerCysPheAenSer 140
Db 361 TATTGCGACAAAGTTGATTTCCCTTGGAGTTGTTCAAAAGACACGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCCGAGTGCATAAACTGTATATAGATATGCAATTCGCAATTCGATTCG 480
Qy 161 ProAenValAenPheGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAenPheAenAenValIleProGluGlyMetAenLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTTAAATGATGATATACCCGAAGGTATGAACTTGAGTTCCCTC 600
Qy 201 IleAlaLeuIleSerAenAenGlyAenTyrThrCysValValThrTyrProGluAenGly 220
Db 601 ATTCGCTTAATTTCAAATAATGGAATTTACACATGTGTGTTACATATCCAGAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAenAla 240
Db 661 CGTAGCTTTTCACTCACGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProValIleHisSerProAenAenHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTTACCTAATGATCAATGTGTGTATGAGAAAGAACGAGGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAenSerArgAenGluVal 280
Db 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGTT 840
Qy 281 TrpTrpThrIleAenPheGlyLysLysProAenAenPheThrIleAenValThrIleAenGlu 300
Db 841 TGGTGGACCAATGATGAAAAAACCCTGATGACATCACTATTGATGTACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAenGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAGACAGAGATGAACCAAGAACTCAGATTTTGAGCATCAAGAA 960
Qy 321 ValThrSerGluAenPheLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCTAAGCGGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAGAAAGTGCCAGCTCCAAGATACACAGTGGAA 1077
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RESULT 11

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US-09-313-942-27
; Sequence 27, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
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; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2730)
US-09-313-942-27

Alignment Scores:
Pred. No.: 3,69e-190 Length: 2733
Score: 1930.00 Matches: 357
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.60% Indels: 0
DB: 3 Gaps: 0
```

US-10-061-727-2 (1-687) x US-09-313-942-27 (1-2733)

```
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAenAla 20
Db 1 ATGGTCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCGAAAGTGTATGCC 60
Qy 21 SerGluArgCysAenPheTrpGlyLeuAenPheMetArgGlnIleGlnValPheGluAen 40
Db 61 TCAGAACGCTCGCATGACTGGGACTAGACCATGAGGCAATCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAenTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACACTCTTTGAATTTCAACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAenPheArgAenGlu 80
Db 181 GCCATTACAGTGGCTTACTCTGATCTGTGTTTGGACTAGGACGACCGGACCTTGAG 240
Qy 81 GluProIleAenPheArgLeuProGluAenArgIleSerLysGluLysAenValLeuTrp 100
Db 241 GAGCAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGAGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAenAenPheThrGlyAenTyrThrCysMetLeuArgAenThrThr 120
Db 301 TTCCGGCCCACTCTCCCTCAATGACACTGGCAACTATACCTGCGATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAenSerCysPheAenSer 140
Db 361 TATTGCGACAAAGTTGATTTCCCTTGGAGTTGTTCAAAAGACACGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCCGAGTGCATAAACTGTATATAGATATGCAATTCGCAATTCGATTCG 480
Qy 161 ProAenValAenPheGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAenPheAenAenValIleProGluGlyMetAenLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTTAAATGATGATATACCCGAAGGTATGAACTTGAGTTCCCTC 600
Qy 201 IleAlaLeuIleSerAenAenGlyAenTyrThrCysValValThrTyrProGluAenGly 220
Db 601 ATTCGCTTAATTTCAAATAATGGAATTTACACATGTGTGTTACATATCCAGAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAenAla 240
Db 661 CGTAGCTTTTCACTCACGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProValIleHisSerProAenAenHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTTACCTAATGATCAATGTGTGTATGAGAAAGAACGAGGAG 780
```



```
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATCTCCCTGACGGTCTATTTTATGTTTCTGATGGATCTCGCAATGAGGT 840
Qy 281 TrpTrpThrIleAspGlyLysProAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCAATTGATGGAAAAAACCTGATGACATCACTATTGATGTCAACATTAAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 320
Db 901 AGTATAAGTCATAGTAGAACAGAAAGTCAAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACTCTGAGGATCTCAGCGCAGCTATGCTGTCATGTAGTAAGTGCACAAAGGCCAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrVal 358
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074
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## RESULT 12

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US-10-282-162-27
; Sequence 27, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2730)
US-10-282-162-27
```

## Alignment Scores:

```
Pred. No.: 3,698-190 Length: 2733
Score: 1930.00 Matches: 357
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.60% Indels: 0
DB: 3 Gaps: 0
```

US-10-061-727-2 (1-687) x US-10-282-162-27 (1-2733)

```
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCTGTGTGTGTAGTAGTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACCTCGATGACTGGGACTAGACACCATGAGGCAAAATCCCAAGTGTGGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCAGCTCGCATCAAGTGCCCACTTTTGAACACTTCTTGAATTTCAACTACAGACACA 180
Qy 61 AlaHisSerAlaGlyLeuThrIleuIleTrpTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGTGTTTGGACTAGGACGACCGGACCTTGAG 240
```

```
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACTTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACCTCCAGTGCCATAAACTGATATAGAATATGSCATTCAGAGGATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180
Db 481 CCAAAATGTAGATGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATAAAATACAGAATTTTAAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATGCTCTTAATTTCAAAATATGGAATACACATGCTGTTGTATACATATCCAGAAAAATGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGCTATAGAAAGAACACAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATCTCCCTGCTACGGTCTATTTTATGTTTCTGATGGATTCTCGCAATGAGGT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCAATTGATGGAAAAAACCTGATGACATCACTATTGATGTCAACATTAAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 320
Db 901 AGTATAAGTCATAGTAAGACAGAAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGCTGTCATGCTAGTAGTCCCAAGGCCAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrVal 358
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074
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## RESULT 13

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US-10-282-162-33
; Sequence 33, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
```



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; SEQ ID NO 33
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-33

Alignment Scores:
Pred. No.: 4,62e-180 Length: 2703
Score: 1833.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 49.96% Indels: 0
DB: 3 Gaps: 0

US-10-061-727-2 (1-687) x US-10-282-162-33 (1-2703)
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 997 TCAGAACGCTCGCATGCTGGGACTAGACACCATGAGGCAATCCAAGTGTTTGAAGAT 1056
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 1057 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTCTTGAATTCACACTACAGACA 1116
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 1117 GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGCGAGGACCGGACCTTGG 1176
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 1177 GAGCCAAATTAACCTCCGCCCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG 1236
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 1237 TTCGGGCCCACTCTCCCTCAATGACACTGGCAACTATACCTGCATGTAAAGGAACTACATA 1296
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
Db 1297 TATTGCGAGCAAGTTGCATTTCCCTTGGAGATTGTTCAAAAAGACAGCTGTTCATATCC 1356
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrIleGlnArgIleThrCys 160
Db 1357 CCCATGAACTCCCGAGTGCATAACTGTATAGATATATGACATTCAGACGATCACTTGT 1416
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 1417 CCAAAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGC 1476
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 1477 TGTATATAAATACAGAAATTTTATATGTAATACCCGAGAGTATGAACCTTGAGTTTCCCTC 1536
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 1537 ATTGCCCTTAATTTCAATAATGAAATATACACATGTGTTGTACATATCCAGAAATGGA 1596
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 1597 CGTACGTTTCATCTCACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATGCA 1656
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 1657 GTGCCCTGTGATCCATTCACCTAATGATCATGTGTTGTATGAGAAAGAACAGAGAG 1716
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 1717 GAGCTACTCATTCCCTGTACGGTCTATTTTGTATTTCTGATGGATCTCGCAATGAGTT 1776
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1777 TGGTGACCACTTGTATGAAAAAACCTGATGACATCACTATTGATGTCACCAATTAAAGAA 1836
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1836
```

```
Db 1837 AGTATAAGTCATAGTAAGACAGAGATGAACAAGAACTCAGATTTTTCAGCATCAAGAAA 1896
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGTAAGTGCCTAAAGGCGAA 1956
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1957 GTTGCCAAAGCAGCCAAAGTGAAGCAGAAAAGTGCCAGCTCCAAGATACACAGTGGAA 2013

RESULT 14
US-10-282-162-35
; Sequence 35, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-35

Alignment Scores:
Pred. No.: 4,64e-180 Length: 2709
Score: 1833.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 49.96% Indels: 0
DB: 3 Gaps: 0

US-10-061-727-2 (1-687) x US-10-282-162-35 (1-2709)
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 997 TCAGAACGCTCGCATGCTGGGACTAGACACCATGAGGCAATCCAAGTGTTTGAAGAT 1056
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 1057 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTCTTGAATTCACACTACAGACA 1116
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 1117 GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGCGAGGACCGGACCTTGG 1176
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 1177 GAGCCAAATTAACCTTCGCCCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG 1236
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 1237 TTCGGGCCCACTCTCCCTCAATGACACTGGCAACTATACCTGCATGTAAAGGAACTACATA 1296
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
Db 1297 TATTGCGAGCAAGTTGCATTTCCCTTGGAGATTGTTCAAAAAGACAGCTGTTCATATCC 1356
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrIleGlnArgIleThrCys 160
Db 1357 CCCATGAACTCCCGAGTGCATAACTGTATAGATATATGACATTCAGACGATCACTTGT 1416
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 1417 CCAAAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGC 1476
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 1477 TGTATATAAATACAGAAATTTTATATGTAATACCCGAGAGTATGAACCTTGAGTTTCCCTC 1536
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 1537 ATTGCCCTTAATTTCAATAATGAAATATACACATGTGTTGTACATATCCAGAAATGGA 1596
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 1597 CGTACGTTTCATCTCACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATGCA 1656
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 1657 GTGCCCTGTGATCCATTCACCTAATGATCATGTGTTGTATGAGAAAGAACAGAGAG 1716
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 1717 GAGCTACTCATTCCCTGTACGGTCTATTTTGTATTTCTGATGGATCTCGCAATGAGTT 1776
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1777 TGGTGACCACTTGTATGAAAAAACCTGATGACATCACTATTGATGTCACCAATTAAAGAA 1836
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1836
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Db 1417 CCAAAATAGATGGATATTTCTTCAGGTGTCAAAACCGACTATCACTTGGTATATGGGC 1476  
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Db 1477 TGTTATAAATAACAGAAATTTTAATAATGTAATPACCGAGGATGAACCTTGAGTTTCCTC 1536  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValTyrProGluAsnGly 220  
Db 1537 ATTGCTTAAATTTCAAAATAATGGAATTTACATGTTGTTTACATATCCAGAAATGGA 1596  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Db 1597 CGTACGTTTCATCTCACCGAGACTCTGACTGTGTAAGGTAGTAGGCTCTCCAAATAATGCA 1656  
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
Db 1657 GTGCCCTCTGTGATCATCTCACTTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
Db 1717 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGGATTCGCGAATGAGGTT 1776  
Qy 281 TrpTrpThrIleAspGlyLysLysProAspIleThrIleAspValThrIleAsnGlu 300  
Db 1777 TGGTGGACCATTTGATGGAAAAAACCTCGATGACATCACATTTGATGTCCACATTAACGAA 1836  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
Db 1837 AGTAAAGTCATAGTAGAACAAGAGTGAACAAGAACTCAGATTTTTCAGCATCAAGAAA 1896  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaAAsqSerAlaLysGlyGlu 340  
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTGATGAGTGTGCAAGTGCACAAAGCGCAA 1956  
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359  
Db 1957 GTTGCCAAAGCAGCCAGGTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGAA 2013

RESULT 15

US-10-282-162-37

; Sequence 37, Application US/10282162

; Patent No. 6927044

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; FILE REFERENCE: REG 203-B-US

; CURRENT APPLICATION NUMBER: US/10/282,162

; CURRENT FILING DATE: 2002-10-28

; PRIOR APPLICATION NUMBER: 09/787,835

; PRIOR FILING DATE: 1999-09-22

; PRIOR APPLICATION NUMBER: PCT/US99/22045

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: PaetSEQ for Windows Version 3.0

; SEQ ID NO 37

; LENGTH: 2709

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-282-162-37

Alignment Scores:  
Pred. No.: 4,648-180 Length: 2709  
Score: 1833.00 Matches: 339  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 49.96% Indels: 0  
Dbs: 3 Gaps: 0

US-10-061-727-2 (1-687) x US-10-282-162-37 (1-2709)

Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40

Db 997 TCAGAACGCTCGCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 1056  
Qy 41 GluProAlaArgIleLysCysPheProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
Db 1057 GAGCGAGCTCGCATCAAGTGGCCACTCTCTTTGAACACTTCTTTGAATAATTCACACTACAGCACA 1116  
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80  
Db 1117 GCCCATTTGAGTGGCTTACTCTGATCTGGTATTGGACTAGCAGGACCCGGAGCTTGAG 1176  
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
Db 1177 GAGCAATTAATCTTCGCTCCCGCTCCCGAGAAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 1236  
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
Db 1237 TTCCGGGCCACTCTCTCAATGACACTGGCAACTATACCTCGCATGTTTAAGGAACAACATACA 1296  
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
Db 1297 TATTGCGAACAAGTTGCAATTTCCCTTCCAGTGTCCAAACCCGACTATCACATTTGGTATATGGGC 1356  
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
Db 1357 CCCATGAAACTCCCGAGTGCATAAACTGTATATAGAAATATGSCATTCACAGGATCACTTGT 1416  
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180  
Db 1417 CCAAATGTAGATGGATATTTTTCCTTCCAGTGTCCAAACCCGACTATCACATTTGGTATATGGGC 1476  
Qy 181 CysTyrLysIleGlnAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Db 1477 TGTTATAAATAACAGAAATTTTAATAATGTAATCCCGAAGGTATGAACTTGAGTTTCCTC 1536  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
Db 1537 ATTGCTTAAATTTCAAAATAATGGAATAATACACATGTGTGTTTACATATCCAGAAATGGA 1596  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Db 1597 CGTACGTTTCATCTCACCGAGACTCTGACTGTGTAAGGTAGTAGGCTCTCCAAATAATGCA 1656  
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
Db 1657 GTGCCCTCTGTGATCATCTCACTTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
Db 1717 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGGATTCCTCGCAATGAGGTT 1776  
Qy 281 TrpTrpThrIleAspGlyLysLysProAspIleThrIleAspValThrIleAsnGlu 300  
Db 1777 TGGTGGACCATTTGATGGAAAAAACCTCGATGACATCACATTTTATGATGTCAACCATTAACGAA 1836  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
Db 1837 AGTAAAGTCATAGTAGAACAAGAGTGAACAAGAACTCAGATTTTTCAGCATCAAGAAA 1896  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaAAsqSerAlaLysGlyGlu 340  
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTGATGAGTGTGCAAGTGCACAAAGCGCAA 1956  
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359  
Db 1957 GTTGCCAAAGCAGCCAGGTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGAA 2013

Search completed: December 14, 2005, 15:40:01  
Job time : 359 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 14, 2005, 15:29:38 ; Search time 1402 Seconds  
(without alignments)  
4052.113 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVVSLFYGIQSDA.....SALAHHTDLSNNDFYIL 687

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*  
-DB=Published Applications NA Main -QWMT=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct  
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-HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10061727.ecgn\_1\_1026\_orunat\_07122005\_113338\_17263/app\_query.fasta\_1.839  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA\_Main:

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8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
1	3667	99.9	2064	6	US-10-061-727-1
2	3281	89.4	2058	6	US-10-061-727-3
3	2591.5	70.6	4724	5	US-10-167-127-9
4	2591.5	70.6	4724	7	US-10-167-127-9
5	2580	70.3	1713	5	US-10-717-597-14
6	2327.5	63.4	3355	6	US-10-215-211-3
7	1938	52.8	2748	6	US-10-205-219-24
					US-10-282-162-51

8	1938	52.8	2748	8	US-10-840-138-21	Sequence 21, Appl
9	1938	52.8	2748	9	US-10-945-068-21	Sequence 21, Appl
10	1938	52.8	2748	10	US-11-056-730-21	Sequence 21, Appl
11	1938	52.8	2748	10	US-11-134-114-51	Sequence 51, Appl
12	1937.5	52.8	2754	6	US-10-282-162-53	Sequence 53, Appl
13	1937.5	52.8	2754	6	US-10-282-162-55	Sequence 55, Appl
14	1937.5	52.8	2754	8	US-10-840-138-23	Sequence 23, Appl
15	1937.5	52.8	2754	8	US-10-840-138-25	Sequence 25, Appl
16	1937.5	52.8	2754	9	US-10-945-068-23	Sequence 23, Appl
17	1937.5	52.8	2754	9	US-10-945-068-25	Sequence 25, Appl
18	1937.5	52.8	2754	10	US-11-056-730-23	Sequence 23, Appl
19	1937.5	52.8	2754	10	US-11-056-730-25	Sequence 25, Appl
20	1937.5	52.8	2754	10	US-11-134-114-53	Sequence 53, Appl
21	1937.5	52.8	2754	10	US-11-134-114-55	Sequence 55, Appl
22	1935	52.7	2703	6	US-10-282-162-39	Sequence 39, Appl
23	1935	52.7	2703	8	US-10-840-138-9	Sequence 9, Appl
24	1935	52.7	2703	9	US-10-945-068-9	Sequence 9, Appl
25	1935	52.7	2703	10	US-11-056-730-9	Sequence 9, Appl
26	1935	52.7	2703	10	US-11-134-114-39	Sequence 39, Appl
27	1935	52.7	2709	6	US-10-282-162-41	Sequence 41, Appl
28	1935	52.7	2709	6	US-10-282-162-43	Sequence 43, Appl
29	1935	52.7	2709	8	US-10-840-138-11	Sequence 11, Appl
30	1935	52.7	2709	8	US-10-840-138-13	Sequence 13, Appl
31	1935	52.7	2709	9	US-10-945-068-11	Sequence 11, Appl
32	1935	52.7	2709	9	US-10-945-068-13	Sequence 13, Appl
33	1935	52.7	2709	10	US-11-056-730-11	Sequence 11, Appl
34	1935	52.7	2709	10	US-11-056-730-13	Sequence 13, Appl
35	1935	52.7	2709	10	US-11-134-114-41	Sequence 41, Appl
36	1935	52.7	2709	10	US-11-134-114-43	Sequence 43, Appl
37	1934	52.7	1077	5	US-10-215-211-5	Sequence 5, Appl
38	1930	52.6	2733	3	US-09-313-942-27	Sequence 27, Appl
39	1930	52.6	2733	3	US-09-935-868-27	Sequence 27, Appl
40	1930	52.6	2733	5	US-10-287-035-27	Sequence 27, Appl
41	1930	52.6	2733	5	US-10-282-162-27	Sequence 27, Appl
42	1930	52.6	2733	8	US-10-840-138-1	Sequence 1, Appl
43	1930	52.6	2733	9	US-10-945-068-1	Sequence 1, Appl
44	1930	52.6	2733	10	US-11-056-730-1	Sequence 1, Appl
45	1930	52.6	2733	10	US-11-134-114-27	Sequence 27, Appl

#### ALIGNMENTS

RESULT 1  
US-10-061-727-1  
; Sequence 1, Application US/10061727  
; Publication No. US20030170632A1  
; GENERAL INFORMATION:  
; APPLICANT: Sims, John E.  
; APPLICANT: Smith, Dirk E.  
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN  
; FILE REFERENCE: 3151-A  
; CURRENT APPLICATION NUMBER: US/10/061,727  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: US 60/244,831  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2064  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2064)  
; OTHER INFORMATION:  
; NAME/KEY: misc feature  
; LOCATION: (1792)..(1792)  
; OTHER INFORMATION: "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.  
US-10-061-727-1

Alignment Scores:  
Pred. No.: 0  
Score: 3667.00  
Length: 2064  
Matches: 687

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.95%	Indels:	0
DB:	6	Gaps:	0

US-10-061-727-2 (1-687) x US-10-061-727-1 (1-2064)

Qy	1	MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyLeuGlnSerAspAla	20
Db	1	ATGACACTTCTGTGGTGTGTAGTGAAGTCTCTACTTTTATGGAATCTCTGCAAGATGATGCC	60
Qy	21	SerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnLeuGlnValPheGluAsp	40
Db	61	TCAGAACGCTGCGATGACTGGGGA CTAGACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT	120
Qy	41	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	60
Db	121	GAGCCAGCTCGCATCAAGTGCCTCTTTGAAACACTCTTTGAAATTTCAACTACAGCACA	180
Qy	61	AlaHisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArgAspLeuGlu	80
Db	181	GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGCAGGACCGGACCTTGAG	240
Qy	81	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp	100
Db	241	GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG	300
Qy	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	120
Db	301	TTCCGGCCCCACTCTCTCAATGACACTGGCAACTATACCTCGATGTTAAGGAAACACTACA	360
Qy	121	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	140
Db	361	TATTGCAGCAAGTGTGCATTTCCCTGGAGTGTGTTCAAAAAGACACTGTGTTCAATTCC	420
Qy	141	ProMetLysGluProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys	160
Db	421	CCCATGAAACTCCCAAGTCATAAACTGTATATAGAATATATGCAATATGCAATTCAGAGGATCACTTGT	480
Qy	161	ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly	180
Db	481	CCAAATGTAGATGGATATTTTTCCTTCCAGTGTCAACCGACTATCACTTGGTATATGGGC	540
Qy	181	CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu	200
Db	541	TGTTATAAAATACAGAAATTTTAAATAATGTAATACCCGAAAGGTATGAACCTTGAGTTTCTC	600
Qy	201	IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValValThrTyrProGluAsnGly	220
Db	601	ATTGCCCTTAATTTCAAAATAAGGAAATTTACACATGTGTGTTTACATATCCAGAAAAATGGA	660
Qy	221	ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	240
Db	661	CGTAGCTTTTCATCTCACCCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA	720
Qy	241	ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	260
Db	721	GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTGTTTACATATCCAGAAAAACAGGAGAG	780
Qy	261	GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	280
Db	781	GAGCTACTCATTTCCCTGTACGGTCTATTTTATGTTTTCTGATGGATTTCTCCATATGAGGTT	840
Qy	281	TrpTrpThrIleAspGlyLysIleProAspAspIleThrIleAspValThrIleAsnGlu	300
Db	841	TGCTGGACCATTTGATGGAAAAAAACCTGATGACATCACTATTGATGTCCACCATTAACGAA	900
Qy	301	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	320
Db	901	AGTATAAGTTCATAGTAGAACAGAGATGAAACAAGAACTCAGATTTTGGACATCAAGAA	960
Qy	321	ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	340



Db 1621 CGTTGGCTCTTCCCTGAGAGGCTCTGAGCGCCAGCTCCGGCTGGAATGAGAGCTGTTCT 1680  
Qy 561 SerGlnSerAspIleSerLeuAspHisValGlnArgArgSerArgLeuLysGluPro 580  
Db 1681 TCTCAGTCTGACATCAGTCTGGATCATGTTTCAG---AGGAGAGTCTGTTTGAAGAGGCC 1737  
Qy 581 ProGluLeuGlnSerSerGluAtgAlaAlaGlySerProAlaProGly\*\*\*MetSer 600  
Db 1738 CCAGAACTCCGAAGCTCAGAGAGGCTGTGGAGCAGAGCCCGCGGACGATGTC 1797  
Qy 601 LysHisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGlu 620  
Db 1798 AAGCACCGAGGAAACCTCAGCAGCCTGTGCTGTGTGTACCTACTACTGTGAAGGAGAA 1857  
Qy 621 AsnHisLeuArgLeuLysSerArgAlaGluIleHisAsnGlnProGlnTrpGluThrHis 640  
Db 1858 AGTCACCTCAGGAGCAGAGCGCGGAGAGTGCACACGCATCCCGAGTGGGAACACAC 1917  
Qy 641 LeuCysLysProValProGlnGluSerGluThrGlnTrpIleGlnAsnGlyThrArgLeu 660  
Db 1918 CTCTGTAAGCTCTCTCCCAAGAGTCTGAAAGTCAGTGGATACAAAATGGCACCCGACC 1977  
Qy 661 GluProProAlaProGlnIleSerAlaLeuAlaLeuHisHisPheThrAspLeuSerAsn 680  
Db 1978 GAA---CCCGCTCCCGCAGATCTCAGCTCTTGCACTCCGCACTTTACAGATTTATCCAAT 2034  
Qy 681 AsnAsnAspPheTyrIleLeu 687  
Db 2035 AACAAATGACTTTTATATCCTTA 2055

## RESULT 3

US-10-167-127-9

; Sequence 9, Application US/10167127  
; Publication No. US20030100031A1  
; GENERAL INFORMATION:  
; APPLICANT: DOWER, STEVEN  
; APPLICANT: DUFF, GORDON W.  
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY  
; FILE OF INVENTION: EVENTS  
; FILE REFERENCE: MSA-026.01 (20974-2601)  
; CURRENT APPLICATION NUMBER: US/10/167,127  
; PRIOR FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: 60/297,305  
; PRIOR FILING DATE: 2001-06-11  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 4724  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-167-127-9

## Alignment Scores:

Pred. No.:	1-586-289	Length:	4724
Score:	2591.50	Matches:	502
Percent Similarity:	86.84%	Conservative:	39
Best Local Similarity:	80.58%	Mismatches:	50
Query Match:	70.63%	Indels:	32
DB:	5	Gaps:	7

US-10-061-727-2 (1-687) x US-10-167-127-9 (1-4724)

Qy 1 MetThrLeuLeuTrpCysValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
Db 207 ATGACACTCTGTGGTGTGTAGTGTCTCTACTTTTATGGAATCCTCGAAAGTGTATGCC 266  
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
Db 267 TCAGAACGCTCGCATGACTGGGACTAGACACCATGAGGCAATCCAAAGTGTTTGAAGAT 326  
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
Db 327 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTTTGAAATTTCAACTACAGCACA 386

Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrTrpThrArgGlnAspArgAspLeuGlu 80  
Db 387 GCCCAATTCAGTCCGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGAGACTTGAG 446  
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
Db 447 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTAAGTAAGGAGAAAGATGTCTGTGG 506  
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
Db 507 TTCGGCCCACTCTCTTCATGACACTGGCACTATACCTGTCATGTTTAAAGAAACACTACA 566  
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140  
Db 567 TATTGAGCAAAAGTTGCTTCCCTTGGAAAGTTGTTCAAAAAGACACAGCTGTTTCAATTCC 626  
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
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Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTyrMetGly 180  
Db 687 CCAATGTAGATGATATTTTCTTCCAGTGTCAACCGACTATCACTTGTGTATATGGGC 746  
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Db 747 TGTATAAAATACAGAAATTTTAATAATGTAATACCCGAGGTATGAATTTGAGTTTCCCTC 806  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
Db 807 ATTGCCCTTAATTTCAATTAATGAAATTAACATGTTGTTTACATATCCAGAAATGGA 866  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Db 867 CGTACGTTTCATCTCACCGAGCTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 926  
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
Db 927 GTGCCCTCTGTATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAGAG 986  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
Db 987 GAGTACTCATTCCTCTGACGGTCTATTTAGTGTTCCTGATGATGATCTCGCAATGAGGTT 1046  
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300  
Db 1047 TGGTGGACCATTCATCGNAANAAAAAACCTGATGACATCACTATTGATGTCCACCATTAAGAA 1106  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
Db 1107 AGTATAAGTCATAGTAGAACAAGATGAAACAAGAACTCAGATTTTGTAGCATCAAGAAA 1166  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
Db 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTGTCATGTAGTAGTGCCTCAAGGCGAA 1226  
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
Db 1227 GTTGCACCAAGCAGCCAAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGGAACTG 1286  
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValIleLeuIleValValTyrHisVal 380  
Db 1287 GCTTGTGGTGTGGAGCCACAGTCTGTGTAGTGGTGTATCTCATTTGTTTACCATTGTT 1346  
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400  
Db 1347 TACTGCTAGAGATGCTCTATTTTACCAGGGCTCATTTTGGAAACAGATGAACCATTTTA 1406  
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420  
Db 1407 GATGAAAGAGATGATGATATTTATGTATCTTATGCAAGGAATCGCGNAGAGAAAGATTTT 1466



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Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAenGluPheGlyTyLysLeuCysIlePhe 440
Db 1467 GTATTACTGACCTCCGTGGAGTTTGGAGATGAATTTGGATACAAGCTGTGCATCTTT 1526
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1527 GACCAGACAGCTGCTCCCTGGGGGAATTGTACAGATGAGACTTTTGAGCTTCATTCCAGAAA 1586
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1587 AGCAGACCCCTCCCTGGTTGTTCTAAGCCCCAACCTACGTGCTCCAGGGAAACCAAGCCCTC 1646
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAenSerIleAlaThrLys----- 496
Db 1647 CTGGAGCTCAAGCTGGGCTA-----GAAATATGGCTCTCGGGGCAACATCAAC 1697
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
Db 1698 GTCAATTTTAGTACAGTACAAAGCTGTGAAGGAAACGAAG-----GTGAAGAGCTGAAG 1751
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1752 AGGGCTAAGACGGTCTCAGGTCATTAAATGGAAGGGGAAATCCCAAGTATCCACAG 1811
Qy 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1812 GCGAGTTCTGGAGCAGCTGCGAGTGGCCATGCCAGTGAAGAAAGTCCCGAGCGGTCT 1871
Qy 554 GlyTrpAenGluSerCysSerSerGlnSerAspIleSerLeuAenPheIleVal-GlnArgAr 573
Db 1872 AGCAGTGTAGCAGCGGCTCTCGTATCA-----TCTTTGAAATAATGTATGAAGGAA 1925
Qy 573 gArg-----SerArgLeuLysGluProProGluLeuG1 584
Db 1926 TAATGAAAGGTTAAAGAAACAAGGGGTGCTCCAGGAAGAAAGTCCCGCCAG----- 1980
Qy 584 nSerSerGluArgAlaAlaGlySerProAlaProGly**MetSerLysHisArgG1 604
Db 1981 -----TCTTCATTCGAGTTTATGGTTTCATAGGCCAAAAATAATGG 2021
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Qy 604 YLysSer 606

Db 2022 TCTAAGC 2028

#### RESULT 4

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US-10-717-597-14
; Sequence 14, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dorner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-14
Alignment Scores:
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Pred. No.: 1.58e-289 Length: 4724
Score: 2591.50 Matches: 502
Percent Similarity: 86.84% Conservative: 39
Best Local Similarity: 80.58% Mismatches: 50
Query Match: 70.63% Indels: 32
DB: 7 Gaps: 7

US-10-061-727-2 (1-687) x US-10-717-597-14 (1-4724)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 207 ATGACACTTCTGTGTGTGTAGTGTCTCTACTTTTATGGAATCTCTCAAGATGTATGCC 266
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 267 TCAGAACCTCCGATGACTGGGGACTAGACACCATGAGGCAATCCAAGTGTGTGAAGAT 326
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 327 GAGCCAGCTGCGCATCAAGTGCCTCTTTTGAACACTTCTTTGAAATTCACACTTACAGCAC 386
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAenArgAspLeuGlu 80
Db 387 GCCCATTCAGCTGCGCTTACTCTGTATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 446
Qy 81 GluProIleAenPheArgLeuProGluAenArgIleSerLysGluLysAspValLeuTrp 100
Db 447 GAGCCAAATTAATCTCCGCTCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGTGTGG 506
Qy 101 PheArgProThrLeuLeuAenAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 507 TTCGGGCCACTCTCTCCTCAATGACACTGGCAACTATACCTGCATGTTTAAGGAACACTACA 566
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 567 TATTGCGAGCAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 626
Qy 141 ProMetLysLeuProValHisLeuLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 627 CCCATGAACATCCCGAGTGCATAAACTGTATATAGAAATATGGCATTCAGAGGATCACTGT 686
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 687 CCAATGTAGATGATATTTTCTTCCAGTGTCAACCGCACTATCCTTGGTATATGGGC 746
Qy 181 CysTyrLysIleGlnAenPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 747 TGTATAAAATACAGAAATTTTAAATAATGTAATACCCGGAAGGTATGAACCTTGAGTTTCCTC 806
Qy 201 IleAlaLeuIleSerAsnAenGlyAsnTyrThrCysValValThrTyrProGluAenGly 220
Db 807 ATTGCCCTTAATTTCAAATAATGGAATAATACACATGTGTGTGTATACATATCCAGAAATGGA 866
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 867 CGTACGTTTCATCTCACACGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 926
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 927 GTGCCCTCTGTGATCCATTCACCTCAATGATCATGTGTGTCTATGAGAAAGAACCCAGGAGAG 986
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 987 GAGTACTCATCTCCCTGTACGGTCTATTTTATGTTTCTGTAGTGGATTCCTCGCAATGAGGTT 1046
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1047 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGTATGTACCCATTAACGAA 1106
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1107 AGTATAAGTCATAGTAGAACAAGAGATGAAACAAGAACTCAGATTTTGTAGCATCAAGAAA 1166
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Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaAsgSerAlaLysGlyGlu 340
Db 1167 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTATGTAGTAGTGCACAAAGGGCAA 1226
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1227 GTTCCCAACAGCCAGGTGAACAGAAAGTGCCAGCTCCAGATACACAGTGGAACTG 1286
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValLleLeuLleValValTyrHisVal 380
Db 1287 GCTTGTGGTTTGAGCCACAGTCTCTAGTGTGATTCTCATTTGTTTACCATGTT 1346
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrLleLeu 400
Db 1347 TACTGGCTAGAGATGGTCTCTATTTACCGGGCTCATTTTGGAAACAGATGAACCATTTTA 1406
Qy 401 AspGlyLysGluTyrAspLleTyrValSerTyrAlaArgAsnAlaGluGluGluLuphe 420
Db 1407 GATGGAAGAAGATGATGATATTTATGTATCTTCACAGGAATGCGGAAGAAGAATTT 1466
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1467 GTATTACTGACCCCTCCGTGGAGTTTGTGAGAAATGAAATTTGGATACAAAGCTGTGCATCTT 1526
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheLleGlnArg 460
Db 1527 GACCGAGACAGTCTGCTCGGGGAATTGTCCACAGATGAGACTTTGAGCTTCATTACAGAAA 1586
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1587 AGCAGAGCCCTCTCGTGTGTTCTTAAGCCCACTACGTCTCCAGGGAACCCAGGCCCTC 1646
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
Db 1647 CTGGAGCTCAAGGCTGGCCTA-----GAAAAATATGGCCTCTCGGGGCAACATCAAC 1697
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyLleLeuGlnLys 516
Db 1698 GTCATTTTAGTACAGTACAAAGCTGTGAAGGAAACGAAG-----GTGAAGAGAGCTGAAG 1751
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1752 AGGCTAAGCGGTGCTCAGCTCATTAATGGAAGGGAAGAAATCCAAGTATCCACAG 1811
Qy 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1812 GGCAGGTTCTGGAAGCAGCTGCAGGTGCCATGCCAGTGAAGAAAGTCCAGCGGTCT 1871
Qy 554 GlyTrpAsnGluSerCysSerGlnSerAspIleSerLeuAspHisVal-GlnArgAr 573
Db 1872 AGCAGTGATGACGAGCGCCTCTCGTATTCA-----TCTTTGAAAAATGTATGAAGGAA 1925
Qy 573 gATg-----SerArgLeuLysGluProProGluLeuG1 584
Db 1926 TAATGAAAAGGTTAAAGAACACAGGGGTGCTCCAGGAAGAAAGAGTCCCCACAG----- 1980
Qy 584 nSerSerGluArgAlaAlaGlySerProProAlaProGly***MetSerLysHisArgG1 604
Db 1981 -----TCTTCATTCCGAGTTTATGTTTTCATAGGCAAAAAATAATGG 2021
Qy 604 yLysSer 606
Db 2022 TCTAAGC 2028
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RESULT 5  
US-10-215-211-3  
; Sequence 3, Application US/10215211  
; Publication No. US20030049255A1  
; GENERAL INFORMATION:  
; APPLICANT: Sims, John E.  
; APPLICANT: Smith, Dirk E.  
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES  
; FILE REFERENCE: 3321-A

```
; CURRENT APPLICATION NUMBER: US/10/215,211  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: US 60/310,789  
; PRIOR FILING DATE: 2001-08-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1713  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1713)  
; OTHER INFORMATION:  
US-10-215-211-3  
Alignment Scores:  
Pred. No.: 6,23e-289 Length: 1713  
Score: 2580.00 Matches: 487  
Percent Similarity: 91.04% Conservative: 31  
Best Local Similarity: 85.59% Mismatches: 45  
Query Match: 70.32% Indels: 6  
DB: 5 Gaps: 3  
US-10-061-727-2 (1-687) x US-10-215-211-3 (1-1713)  
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
Db 1 ATCACACTCTCTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60  
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
Db 61 TCAGAACGCTCGCATGACTGGGACTAGACACCATGAGGCAAAATCCCAAGTGTTTGAAGAT 120  
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAAACACTTCTTGAAATTCACATCAGCAC 180  
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80  
Db 181 GCCCATTCAGTCGCCCTTACTCTGACTGTGTATGGACTAGGACGACCGGACCTTGAG 240  
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
Db 241 GAGCCCAATTAACTTCCGCCCTCCCGCAGAACCGCATTTAGTAAGGAGAAAGATGTCTGTGG 300  
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
Db 301 TTCGGCCCCACTCTCTCAATGACACTGGCACTATACCTTGCATGTTTAAAGAACACATACA 360  
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420  
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
Db 421 CCCATGAAACTCCAGTGCATAAACTGTATATAGAATATGCAATATGCAATTCAGAGATCAGTGT 480  
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180  
Db 481 CCNAATGTAGATGGATATTTTCTTCCAGTGTCAAACCCGACTATCATCTTGATATATGGGC 540  
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Db 541 TGTATATAAATACAGAAATTTAATAATACCCGAGGTATGAATTCAGTTCCTTCCTC 600  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
Db 601 ATTGCTCTTAATTTCAAAATAATGGAATATACACATGTGTGTTTACATATCCAGAAAAATGGA 660  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Db 661 CGTACGTTTCTTCACTCACCAGGACTGTGACTGTAAAGTAGTAGGCTCTCCAAAAAATGCA 720
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Qy 241 ValProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTCGTACGGTCTATTTAGTTTCTGTGATGGATTCCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysValProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGACCATTTGATGGAAAAAACCTGATGACATCATATGTATGTACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAGTCATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCTATGCTAGAAAGTGCACAAAGCGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTCCCAAGCAGCAAGGTGACCGAGAAAGTGCAGCTCCAGATACACAGTGGAACTG 1080
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
Db 1081 GCTTGTGGTTTGGAGCCACAGTCTCTGCTAGTGTGATCTCANTGTGTGTTACATGTT 1140
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1141 TACTGGCTAGAGATGGTCTATTTACCGGCTCATTTTGGACAGATGAACCATTTTA 1200
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db 1201 GATGAAAGAGATGATATATTTATGTATCTCTATCAAGGAATGCGGAAGAGAAAGATTT 1260
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1261 GTTTTACTGACCTCCGCTGGAGTTTGGAGATGATTTGGATCAAGCTGTGATCTTT 1320
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1321 GACCGAGACATCTGCTCGCTGGGGAATTGTACAGATGAGACTTTTGAGCTTCATTCAGAA 1380
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1381 AGCAGACGCTCTCGTGGTTTCTAAGCCCAACTACGTGTCTCAGGGAACCAAGCCCTC 1440
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThr--LysLeuIleVal 499
Db 1441 CTGAGCTCAAGCTGGCTGAGAAATATGGGCTCTCGGGCAACATCAACGTCATTTTA 1500
Qy 500 ValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLysGluSer-- 518
Db 1501 GTACAGTACAAAGCTGTGAAGAAACGAAG-----GTGAAGAGCTGAGAGGGCTAAG 1554
Qy 519 -----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPhe 536
Db 1555 ACGGTGTCTACGGTCAATTAATGGAAGGGGAAAAATCCAAAGTATCCACAGGGCAGGTT 1614
Qy 537 TrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSerGlyTrpAsn 556
Db 1615 TGGAAAGCAGCTGCAAGGTGCCATGCCAGTGAAGAAAGTCCAGGGCGGTCTAGCAGTGAAT 1674
Qy 557 GluSerCysSerSerGlnSerAspIle 565
Db 1675 GAGCAGGCGCTCTCGTATTTCATCTTG 1701
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RESULT 6

US-10-205-219-24

; Sequence 24, Application US/10205219

; Publication No. US20030138803A1

## GENERAL INFORMATION:

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; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 3355
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Second subunit of the interleukin 1 receptor complex
US-10-205-219-24
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## Alignment Scores:

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Pred. No.: 4.97e-259 Length: 3355
Score: 2327.50 Matches: 443
Percent Similarity: 83.36% Conservative: 73
Best Local Similarity: 71.57% Mismatches: 76
Query Match: 63.44% Indels: 28
DB: 6 Gaps: 8
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US-10-061-727-2 (1-687) x US-10-205-219-24 (1-3355)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 135 ATGGGACTTCTGTGGTATTTGATGAGTCTGTCTTCTATGGGATCCTGCAGAGTCATGCT 194
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 195 TCGGAGCGCTGTGATGACTCGGGACTAGATACCATCGACAAATCCAAGTGTGTTGAAGAT 254
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 255 GAGCGGCTCGAATCAAGTCCCTCTTTGAACACTTCTCTGAAGTACAACTACAGCACT 314
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 315 GCCCATTCCTCTGGCTTACCTTGATCTGTGTACTGGACCAAGGCAAGCCGGGACTGGAG 374
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 375 GAGCCCATTAACCTCCGCTCCAGAGATCCGATCAGTAAGGAGAAAGATGTCTCTGG 434
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 435 TTCGGGCCCACTCTCTCAATGACCGGCAATATACACTTGCATGTGTGAGGAACACAACT 494
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 495 TACTGCAAGCAAGTTGCAATTCCTTCCCTGGAAGTGTTCAGAAAGGACAGCTGTTCAATTCT 554
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 555 GCCATGAGATTCACAGTGCACAGATGTATATTGNACATGGCATTCATAGATCACATGT 614
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 615 CCAAAATGTAGACGATACTTCTCTCCAGTGTCAAACCATCCGGTCACTTGTGTATAAGGGT 674
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 675 TGTACTGAAAATAGTGGACTTTCATATGTATACCCCGAGGGCATGAACCTTGAGCTTTTC 734
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
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Db 735 ATCCCTTGGTTTCAAATAACGGAATTTACACATGTGTGGTTTACATATCTCTGAAACCGGA 794
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValValGlySerProLysAsnAla 240
Db 795 CGTCTCTTTACCTCACCAGGACTGTGACTGTAAGGTGTGGCTCACCNAAGGATGCA 854
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 855 TTGCCACCCAGATCTATTCTCCAATACCGCTGTCTATGAGAAAGAACACGAGGAG 914
Qy 261 GluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 915 GAACGTGTTATTCCTCCAAAGCTATTTCAGTTTCAITATGAGACTCCCAATAGAGTC 974
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 975 TGGTGGACCATTTGATGAAAGAGCCTGATGAGTCACAGTCACATCAGCATCTATTATGAA 1034
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1035 AGTGTAAAGTTATTCTTCAACGGAAGATGAAACAGGACTCAGATTTTGGACATCAAGAA 1094
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCyeHisAlaArgSerAlaLysGlyGlu 340
Db 1095 GTCAACCCGAGGATCTCAGCGCACTATGTCTCATCTCGAATACCAAGGGGAA 1154
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1155 GCTGAGCAGGCTGCCAGGTGAAACAGAGAAATCATACCACCAAGGTACACAGTAGAATC 1214
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuLeuValValTyrHisVal 380
Db 1215 GCCTGTGGTTTGGAGCACCGCTTTCTCGTAGTGTCTCATTTGTGGTTTACCATGTT 1274
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1275 TACTGCTGAGATGGTCTCTTTTACCGAGCTACTTTTGGAAACAGATGAACAATCTTT 1334
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db 1335 GATGGAAGCAGTATGATATTTATGTTTCTATGCAAGAAATCTGGAAGAGGAAATTT 1394
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1395 GTCTGTCTGACGCTGCGTGAGATTGGAGAATGAGTTTGGATACAAAGCTGTGCATCTTC 1454
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1455 GACAGAGACAGCTGCTGGGGAATGTGCAGATGAGACCTGTGAGCTTTCATTTCAGAA 1514
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1515 AGCAGACGACTCTCGTGTGCTTAACTAGTCCCACTACGTGCTCCAGGGAACACAAAGCCCTC 1574
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys 496
Db 1575 CTGGAGCTCAAGCTGCGCTTA-----GAAATATATGCTCTCCCGGGCAACATCAAC 1625
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
Db 1626 GTCATTTTATGTGCTACAAAGCTGTGAAGGACATGAAG-----GTGAAAGAGCTGAAG 1679
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1680 CGGGCTAAGACGCTGCTCAGGCTCAATTAATGGAAGAGAGAAATCCAAGTATCTCTCAG 1739
Qy 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1740 GGCAGGTTCTGGAAGCAGTTGACGTGGCCATGCCAGTGAAGAG-----AGTCCC 1790
Qy 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArg 573
```

```
Db 1791 AGGTGCTCT-----AGCAATGACACAGAGG-TCTCTCTCTACTCATCCCTGAAAAA 1840
Qy 574 ArgSerArgLeuLysGluProGluLeuGlnSerSerGluArgAlaAlaGlySer--- 592
Db 1841 CGTATGAA-----GGAGAGAGTGGGGGTACAAAGAACAAAGCGGTTCATGG 1888
Qy 593 -----ProProAla-ProGly***MetSerLysHisArgGlyLysSerSer 607
Db 1889 GAGGAAGGGCCCCCTCTTCTTAGGCTGTGCTTTCATAGACAGAAAAAGAGT 1943

RESULT 7
US-10-282-162-51
; Sequence 51, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-51

Alignment Scores:
Pred. No.: 8,27e-214 Length: 2748
Score: 1938.00 Matches: 432
Percent Similarity: 63.42% Conservative: 50
Best Local Similarity: 56.84% Mismatches: 141
Query Match: 52.82% Indels: 140
DB: 19 Gaps: 19

US-10-061-727-2 (1-687) x US-10-282-162-51 (1-2748)
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTCTCTGTGGTGTGTAGTGTACTCTACTTTTATGGAATCTCGCAAGTGTATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGGATGACTGGGGACTTAGACACCATGAGGCAATCCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAAACACTCTTTGNAATTCACCTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTATTGGACTAGGCAGGACCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCAATTAATCTTCGCCCTCCCGAGAACCCGCAATTAGTAGAGAGAAAGATGTGCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCTCTCAATGACACTGCGCACTATACCTGTCATGTTTAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTTCAAAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
```

Db 421 CCCATGAACCTCCAGTCATATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480  
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180  
Db 481 CCAATGTAGATGGATATTTCTTCCAGTGTCAAAACCGACTATCATTGGTATATATGGC 540  
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Db 541 TGTATAAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAATCTGAGTTTCCTC 600  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValTyrProGluAsnGly 220  
Db 601 ATTGCTCTAAATTTCAAAATTAAGAAATATACATGTGTGTGTATACATATCCAGAAATGGA 660  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Db 661 CGTAGCTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAANAATGCA 720  
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
Db 721 GTGCCCTGTGTATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
Db 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTATAGTTTCTGTAGTGAATTCGCAATGAGGTT 840  
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300  
Db 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCATATTGATGTACCATTAAACGNA 900  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
Db 901 AGTATAAGTCATAGTAGAACAGAGAGAGTGAACAGAACTCAGATTTTGAGCATCAAGAAA 960  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTCATGTAGAAAGTGCACAAAGGCGAA 1020  
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
Db 1021 GTTGCCAAAGCAGCCAGGTGAGCAGAGAAAGTGCAGCTCCAGATACACAGTGCACACA 1080  
Qy 361 -----AlaCysGlyPhe----- 364  
Db 1081 GGGGTGCCAGAGCTGCGGTTCGTGGGAGGCATTACAAGCGGAGTTTCAGGCTGGAA 1140  
Qy 365 GlyAlaThrValLeuLeuValValIleLeuLeuValValTyrHisValTyrTrpLeuGlu 384  
Db 1141 GGGGAGCCCTGTAGCCCTGAGGTCGCCCGAGGTG-----CCCTACTGTTGTGG 1188  
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393  
Db 1189 GCCTCTGTACGCCCGCATCACTGATGCGCATAAATATGACTCTGTAGGACGGTC 1248  
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412  
Db 1249 CCAGGAGAAAGAGACACCGATGTGGCCAGGACGGTGTCTGTGGCTTCTCCAGCC 1308  
Qy 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432  
Db 1309 TTGCAGGAGGACTCTGGCACCTAGCTGTGCATCTAGAAATGTCTTCTACTGTGCAAAA 1368  
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452  
Db 1369 ATGTCCATTGAGTCAGAGTTTGTAG-----AATACA---GAT 1404  
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467  
Db 1405 GCTTCTCTGCGCTTCATCTCATCCGCCAAATTTTAACTTGTCAACCTCTGGGGTATTA 1464  
Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487  
Db 1465 GTATGCCCTGCAC-----CTGAGTGAATTC----- 1488

Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507  
Db 1489 -----ACCCGTGACAAAACCTGAGTGAAGATTCAATGTTACAG----- 1527  
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527  
Db 1528 -----GATTCTCTCTTTTGGATAAAGACAATGAGAAATTTCTTAAGTGTGAGGGGACC 1581  
Qy 528 LysSer----- 529  
Db 1582 ACTCATTACTCTGACAGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGCTCTG 1641  
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544  
Db 1642 ACATTTCCCATGAGGCCAGCAATACATCACTAGGAGTATTGAGCTACGATCAAG 1701  
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552  
Db 1702 AAAAAAAGAGAGACCATTTCTGTGATCATTTCCCTCCCTCAAGACCATATCAGCTTCT 1761  
Qy 553 SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572  
Db 1762 CTGGGG-----TCAAG-AC TGACAATCCCATGTAAGGTGTTTCTGGG 1802  
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587  
Db 1803 AACCGGCACACCTTACCACCATGCTGTGGTGGAGCGGCCAATGACACCCACATAGAGAG 1862  
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly\*\*\*MetSerLys----- 601  
Db 1863 CGCTACCCGGAGGCGCGTGACCGAGGGGCCACGCCAGGAATATTTCAGAAAAATAATGA 1922  
Qy 602 -----HisArgGlyLysSerSerAla 608  
Db 1923 GAATACATTGAAGTGCCATTGATTTTGTGATCTGTGCACAGAGAGGATTTCACATGGA 1982  
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628  
Db 1983 TTTTAAATGTGTGTCTCATTAATACCTGAGTT-TTCAGACACTAGCAGCACCACAGTCAAGG 2041  
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648  
Db 2042 AAGCCTCTCCAGCTTCTCCGAGAC-AAAACTCACACATGCCACCGTGCACGACCT 2100  
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666  
Db 2101 GAA-----CTCCTGGGGGACCGCTCAGTCTTCTCTTCCCCCCCCAAACCCCAAG 2148

RESULT 8  
US-10-840-138-21  
; Sequence 21, Application US/10840138  
; Publication No. US20040224893A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Li-Heien  
; APPLICANT: Lin, Hsin Chieh  
; APPLICANT: Karow, Margaret  
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia  
; FILE REFERENCE: REG 207A  
; CURRENT APPLICATION NUMBER: US/10/840,138  
; CURRENT FILING DATE: 2004-05-06  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 2748  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-840-138-21

Alignment Scores: 8.27e-214 Length: 2748  
Pred. No.: 1938.00 Matches: 432  
Score: 63.42%  
Percent Similarity: 63.42%

Best Local Similarity: 56.84%			Mismatches: 141				
Query Match: 52.82%			Indels: 140				
DB: 8			Gaps: 19				
US-10-061-727-2 (1-687) x US-10-840-138-21 (1-2748)							
Qy	1	MetThrLeuLeuTrrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla	20	Qy	341	ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu	360
Db	1	ATGGTGTCTCTGTGGTGTAGTAGTCTCTACTTTTATGGAATCTCTCAAAGTATGCC	60	Db	1021	GTTGCCAAAGACGCCAAGGTGAAGCAGAAAGTCCAGCTCCAAGATACACAGTGCACACA	1080
Qy	21	SerGluArgCysAspAspTrrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp	40	Qy	361	-----AlaCysGlyPhe-----	364
Db	61	TCAGAACGCTGCGCATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGAAGAT	120	Db	1081	GGGGCTGCCAGAGCTGCCGGTTTCGTGGAGGCATTACAAGCGGGAGTTCAGGCTGGAA	1140
Qy	41	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	60	Qy	365	GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu	384
Db	121	GAGCCAGCTCGCATCAAGTGCCTCTTTGAACACTCTTTGAAATTTCAACTACAGACA	180	Db	1141	GGGAGCCTGTAGCCCTGAGGTGCCCCAGGTG-----CCCTACTGGTGTGG	1188
Qy	61	AlaHisSerAlaGlyLeuThrLeuIleTrrpTyrTrpThrArgGlnAspArgAspLeuGlu	80	Qy	385	MetValLeuPheTyrArgAlaHisPhe-----	393
Db	181	GCCCATTTAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG	240	Db	1189	GCCTCTGTGAGCCCGCCGCATCAACCTGCATGGCATAAAAATGACTCTGTAGGACGGTC	1248
Qy	81	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrrp	100	Qy	394	---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla	412
Db	241	GAGCCAAATTAACCTTCGCTCCCGCAGAACCCGCATTAGTAAGGAGAAAGATGTCTGTGG	300	Db	1249	CCAGGAGAAAGACAGACACGGATGTGGGCCCGAGAGCGTCTCTGTGGCTTCTGCCAGCC	1308
Qy	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	120	Qy	413	ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu	432
Db	301	TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTGTAAGGAACTACA	360	Db	1309	TTGCAGGAGGACTCTGGCACCTACGTCTGCACCTACTAGAAATGCTTCTTACTGTGACAAA	1368
Qy	121	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	140	Qy	433	PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu	452
Db	361	TATTGCAGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC	420	Db	1369	ATGTCCATTGAGCTCAGAGTTTTTTGAG-----	1404
Qy	141	ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys	160	Qy	453	AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal	467
Db	421	CCCATGAATCCCGAGTGCATAAATCTGATATAGAATATGGCAATTACAGAGATCACTGT	480	Db	1405	GCTTTTCTCGCGTTCATCTCATACCCGCAAAATTTTAACTTGTCAACCTCTGGGGTATTA	1464
Qy	161	ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrrpTrrpMetGly	180	Qy	468	LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal	487
Db	481	CCAAATGTAGATGGATATTTTCTTCCAGTGTCAACCGACTATCACTTGGTATATGGGC	540	Db	1465	GTATGCCCTGAC-----CTGAGTGAATTC-----	1488
Qy	181	CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu	200	Qy	488	MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis	507
Db	541	TGTTATAAATAACAGAAATTTAATATGTAATACCCGAAGTATGAACCTTGAGTTTCCCTC	600	Db	1489	-----ACCGTGACAAATCGACTGAGAGTCAATGGTACAAG-----	1527
Qy	201	IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly	220	Qy	508	ProHisProGlyIleLeuGlnLysGluSerValSerPheValSerTrpLysGlyGlu	527
Db	601	ATTGCCCTTAATTTCAAATAATGGAATTTACACATGTGTGTTGTATACATATCCAGAAATGGA	660	Db	1528	-----GATTTCTTCTTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC	1581
Qy	221	ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	240	Qy	528	LysSer-----	529
Db	661	CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA	720	Db	1582	ACTCACTTACTCGTACACGATGTGGCCCTGGAGAGATGCTGGCTATTACCCGCTGTCTCTG	1641
Qy	241	ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	260	Qy	530	-----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu---	544
Db	721	GTGCCCTGTGATTCATTCACCTAATGATCATGTGTGCTATGAGAAAGAACCCAGAGAG	780	Db	1642	ACATTTGCCCATGAGGCCAGCAATACACATCACTAGGAGTATTGAGCTACGCATCAAG	1701
Qy	261	GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	280	Qy	545	-----ProLeuArgSerLeuSerAlaSer	552
Db	781	GAGCTACTCATTTCCCTGTACGGTCTATTTTATGTTTCTGATGGATTTCTCGCAATGAGGTT	840	Db	1702	AAAAAAAAGAGAGACCATTTCTGTGATCATTTTCCCCCTCAAGACCATATCAGCTTCT	1761
Qy	281	TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu	300	Qy	553	SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg	572
Db	841	TGTTGGACCATTTATGGAAGAAACCTGATGACATCACTATTGATGTCACCATTAACGAA	900	Db	1762	CTGGGG-----TCAAG-ACTGACAATCCCATGTAAAGGTGTTTCTCTGGG	1802
Qy	301	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	320	Qy	573	ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu	587
Db	901	AGTATAGTCATAGTAAACAGAGAGATGAAACAAAGAACTCAGATTTTGTAGCATCAAGAA	960	Db	1803	AAACGGCACACCTTAAACCCCATGCTGTGTGGTGGACGGCCCAATGACACCCACATAGAGAG	1862
Qy	321	ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	340	Qy	588	ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys-----	601
Db	961	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTGCATGCTAGAGTGCCTCAAGGCGAA	1020	Db	1863	CGCTTACCCTCCGGGAGGCCGCGTGCACGAGGGGCCACCGCCAGGAATATTCAGAAAAAATAATGA	1922
Qy				Qy	602	-----HisArgGlyLysSerSerAla	608
Db				Db	1923	GAACTACATTGAAGTCCCATTTTGTGATCTCTGTGCACAGAGAGGATTTGACATGGA	1982



Qy 609 ThrCysArgCysCysValThrTyrCysGluGluGluAenHisLeuArgAsnLysSerArg 628  
|||  
Db 1983 TTTTAAATGTGTGTCCTAATACCTGAGTT-TTCAGACACTACGCACACAGTCAGTCAAGG 2041  
|||  
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648  
|||  
Db 2042 AGCCTCTCCAGTGTTCGGAGAGAC-AAAACCTCACATGCCACCGCCACCGCACCT 2100  
|||  
Qy 649 SerGluThrGlnTrpIleGlnAenGlyThrArg-----LeuGluProProAlaProGln 666  
|||  
Db 2101 GAA-----CTCCTGGGGGACCGTCAGTCTTCCTCTTCCCTCCCAACCCCAAG 2148  
|||  
RESULT 9  
US-10-945-068-21  
; Sequence 21, Application US/10945068  
; Publication No. US20050129685A1  
; GENERAL INFORMATION:  
; APPLICANT: Jingtai Cao  
; APPLICANT: Stanley J. Wiegand  
; TITLE OF INVENTION: USE OF IL-1 BLOCKERS TO PREVENT CORNEAL INFLAMMATION  
; FILE REFERENCE: REG 208A  
; CURRENT APPLICATION NUMBER: US/10/945,068  
; CURRENT FILING DATE: 2004-09-20  
; PRIOR APPLICATION NUMBER: 60/503,854  
; PRIOR FILING DATE: 2003-09-18  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 2748  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-945-068-21

Alignment Scores:  
Pred. No.: 8.27e-214 Length: 2748  
Score: 1938.00 Matches: 432  
Percent Similarity: 63.42% Conservative: 50  
Best Local Similarity: 56.84% Mismatches: 141  
Query Match: 52.82% Indels: 140  
DB: 9 Gaps: 19

US-10-061-727-2. (1-687) x US-10-945-068-21 (1-2748)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
|||  
Db 1 ATGTGCTTCTGTGTGTAGTAGTCTCTACCTTTATGGAATCCTGCCAAGTGTATGCC 60  
|||  
Qy 21 SerGluArgCysAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
|||  
Db 61 TCAGAACGCTCGATGACTGGGACTAGACACCATGAGGCAATCCAAAGTGTGTAAGAT 120  
|||  
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
|||  
Db 121 GAGCAGCTCCATCAAGTGCCTCTTTTGAACACTTCTTGAACACTTCTTGAACACTACAGCACA 180  
|||  
Qy 61 AlaHisSerAlaGlyLeuLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80  
|||  
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTGGACTAGGACGAGCGGACCTTTGAG 240  
|||  
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
|||  
Db 241 GAGCCATTAATCTTCGGCTTCCCGAGAACCGCATTAGTAGGAGAAAGATGTCTGTGG 300  
|||  
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
|||  
Db 301 TTCGGGGCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACACTACA 360  
|||  
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
|||  
Db 361 TATTGACAGCAAGTGTGATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTC 420  
|||  
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
|||

Db 421 CCCATGAACCTCCAGTGCATAAACTGTATATAGATATATGCAATTCAGAGATCACTTGT 480  
|||  
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180  
|||  
Db 481 CCAAATGTAGATGATATTTTCTTCCAGTGTCAAAACCGACTATACACTTGTGTATATGGGC 540  
|||  
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLysSerPheLeu 200  
|||  
Db 541 TGTATATAAATACAGAAATTTAATAAGTATATACCCGAGGTATGAACCTTGTCTTCCTC 600  
|||  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
|||  
Db 601 ATTGCCTTAATTTCAAATAATGGAATTTACATATGTGTGTATACATATCCAGAAATGGA 660  
|||  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValGlySerProLysAsnAla 240  
|||  
Db 661 CGTACGTTTCACTCACCAGGACTCTGACTGTAAGGTAGTGGCTCTCCAAAAAATGCA 720  
|||  
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
|||  
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 780  
|||  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
|||  
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGGTT 840  
|||  
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300  
|||  
Db 841 TGGTGGACCATTTGATGAAAAAACCCTGATGACATCACTATTGTATGTCAACATTAAACGA 900  
|||  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
|||  
Db 901 AGTATAAGTCTATAGTACAGACAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960  
|||  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
|||  
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGCTAGAAAGTGCACAAAGCGCAA 1020  
|||  
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
|||  
Db 1021 GTTCCCAAGCAGCCAAAGGTGAAGAGTGCAGTCCCAAGATACACAGTGCACACA 1080  
|||  
Qy 361 -----AlaCysGlyPhe----- 364  
|||  
Db 1081 GGGGCTCCAGAGCTCCCGTTCTGTGGGAGGCAATTACAAGCGGGAGTTGAGGCTGAAA 1140  
|||  
Qy 365 GlyAlaThrValLeuLeuValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384  
|||  
Db 1141 GGGGAGCTGTGTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188  
|||  
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393  
|||  
Db 1189 GCCTCTGTACGCCCGCCCATCAACCTGCATAGGCATAAAAATGACTCTGTAGGACGGTC 1248  
|||  
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412  
|||  
Db 1249 CCAGGAGAAAGAGACACCGATGTGGCCCGCAGGCGGTCTCTGTGTCTTCCAGGCC 1308  
|||  
Qy 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432  
|||  
Db 1309 TTGCAGGAGGACTCTGGCACCCTACGCTCTGCACCTACTAGATAAATGCTTCTTACTGTGACAAA 1368  
|||  
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452  
|||  
Db 1369 ATGTCCATTGAGCTCAGAGTTTGTAG-----AATACA---GAT 1404  
|||  
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467  
|||  
Db 1405 GCTTTCCTGCGGTTCATCTCATCCCGCAAAATTTTAACCTTGTCAACCTCTGGGGTATTA 1464  
|||  
Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487  
|||



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Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValGluTyrArgProLeuGluHis 507
Db 1489 -----ACCCGTGACAAACTGACGTGAAGATTCAATGGTACAAG----- 1527
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTTCTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGGACC 1581
Qy 528 LysSer----- 529
Db 1582 ACTCACTTACTCTGACGATGTGGCCCTGGAAGATCTGGCTATTACCCGCTGTGCTCTG 1641
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTTGCCATGAAGCCAGCAATACAACATCACTAGGAGTATTGAGCTACGCATCAAG 1701
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAAGAGACCATTCCTGTGATCATTTCCCCCTCAAGACCATATCAGCTTCT 1761
Qy 553 SerGlyTrpAsnGluSerCysSerGlnSerAspIleSerLeuAspHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ACTGACAAATCCCATGTAAGTGTTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
Db 1803 AACCGGCACACCCCTTAACCAACCATGCTGTGTGGTGGACGGCCAATGACACCCACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCCTACCGGGAGCGCGGTGACCGAGGGGCCACGCGCAAGATAATPCAGAAAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACATCAATTGAAGTGCATTTGATTTGATCTGTGCACAGAGAGATTGTCACATGGA 1982
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAAATGTGTGTCCATAATACCCCTGAGTT- TTCAGACACATAGCCACACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 AAGCCTCCTCCAGCTTCTCCGGAGAC-AAAACTCACACATGCCACCGTCCCGCCAGCACCT 2100
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666
Db 2101 GAA-----CTCCTGGGGGGACCGTCACTGCTTCTCTTCCCCCAAAACCCAAAG 2148
```

## RESULT 10

```
US-11-056-730-21
; Sequence 21, Application US/11056730
; Publication No. US20050197293A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Neil
; APPLICANT: Stahl, Neil
; APPLICANT: Radin, Allen
; APPLICANT: Weinstein, Steven
; APPLICANT: Calaprice, Denise
; APPLICANT: Karow, Margaret
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Use of an IL-1 Antagonist for Treating Arthritis
; FILE REFERENCE: 203G
; CURRENT APPLICATION NUMBER: US/11/056,730
; CURRENT FILING DATE: 2005-02-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

## ; OTHER INFORMATION: Synthetic

US-11-056-730-21

## Alignment Scores:

Pred. No.:	8.27e-214	Length:	2748
Score:	1938.00	Matches:	432
Percent Similarity:	63.42%	Conservative:	50
Best Local Similarity:	56.84%	Mismatches:	141
Query Match:	52.82%	Indels:	140
DB:	10	Gaps:	19

US-10-061-727-2 (1-687) x US-11-056-730-21 (1-2748)

```
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGTCGCTTCTGTGGTGTGTAGTGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAAACGCTGCGATGACTGGGACCTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAATTCACATACACACACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCCTTACTCTGTATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACCTTCCGCTCCCGAGAACCGCATTTAGTAAGAGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTTGGAAGTTGTTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCATGAAACTCCCATGTCATAAATCTGTATATAAGATATGGCATTGAGAGATCATTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAAATGTAGATGGATATTTCTCTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAAATACAGAAATTTTAATAATGTAATACCCGAAAGGTATGAACTTTGAGTTTCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAAATTTCAAATAATGGAATATACACATGTGTGTATACATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCACTCCACGAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTGTGACGGTCTATTATTAGTATTTCTGATGATGATTCCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGGAAAAAANAACCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
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Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100  
Db 241 GAGCAATTAATCTCCCGCTCCCGAGAACCGCATTTAGTAAGAGAAAGATGTCTGTGG 300  
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
Db 301 TTCCGGCCCACTCTCCTCNATGACACTGGCAACTATACCTGCATTTTAAGGAACACTACA 360  
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
Db 361 TATTGCAGCAAGTTGCATTTCCCTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420  
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
Db 421 CCCATGAATCCCGAGTGCATAAATCTGATATAGATATATGGCATTTACAGAGATCACTGT 480  
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTyrMetGly 180  
Db 481 CCAATGTAGATGATATTTCTTCCAGTGTCAACCGACTATCACTTGGTATATGGC 540  
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAAGTATGAACCTTGAGTTTCCCTC 600  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
Db 601 ATTGCCCTTAATTTCAAAATAATGGAATTTACACATGTGTTGTATCATATCCAGAAAATGGA 660  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Db 661 CGTACGTTTCATCTCACAGAGACTCTGACTGTAAAGTAGTAGGCTCTCCAAAATAATGCA 720  
Qy 241 ValProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 780  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
Db 781 GAGTACTCATTCCTGTACGGTCTATTTAGTTTCTGATGGATTCCTGCAATGAGGTT 840  
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300  
Db 841 TGGTGGACCAATTGATGGAAAAAACCCTGATGACATCATATTGATGACCATTTAAGAA 900  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
Db 901 AGTATAAGTCATAGTAAACAGAGAATGAAACAAGAACTCAGATTTTGACCATCAAGAA 960  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
Db 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGTCATGCTAGAAGTGCAAAGCGAA 1020  
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
Db 1021 GTTGCCAAAGACGCAAGGTGAAGCAGAAAGTCCAGCTCCAAAGATACACAGTGCACAA 1080  
Qy 361 -----AlaCysGlyPhe----- 364  
Db 1081 GGGGCTGCCAAGAGCTGCCGGTTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140  
Qy 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384  
Db 1141 GGGGAGCCTGTAGCCCTGAGGTTGCCCGAGGTG-----CCCTACTGGTTGTGG 1188  
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393  
Db 1189 GCCTCTGTAGCCCCCGCATCACTGACATGCGATGCAATAAATGACTCTGCTAGGACGGTC 1248  
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412  
Db 1249 CCAGGAGAAGAGAGACACGAGTGTGGCCCGCAGGAGCGGTCTCTGTGCTTCTGCCAGCC 1308

Qy 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432  
Db 1309 TTGCAGGAGGACTCTGGCAGCTACGTCTGCACCTACTAGAAATGCTTCTTACTGTGACAAA 1368  
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452  
Db 1369 ATGTCATTGAGCTCAGAGTTTITGAG-----AATACA---GAT 1404  
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467  
Db 1405 GCITTCCTGCGGTTCATCTCATACCCGCAAAATTTAACTTGTCAACCTCTGGGGTATTA 1464  
Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487  
Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488  
Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507  
Db 1489 -----ACCGTGACAAAACCTGAGTGAAGATCAATGGTACAAG----- 1527  
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527  
Db 1528 -----GATTCTCTCTTTTGGATAAAGACAATCAGAAATTTCTAAGTGTGAGGGGACC 1581  
Qy 528 LysSer----- 529  
Db 1582 ACTCACTTACTCGTACACGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGCTCTG 1641  
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544  
Db 1642 ACATTTGCCCATGAAGCCAGCAATACAACATCACTAGGAGTATTGAGCTACGCATCAAG 1701  
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552  
Db 1702 AAAAAAAGAGAGACCATTCCTGTGATCATTTCCCCCTCAAGACCATATCAGCTTCT 1761  
Qy 553 SerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572  
Db 1762 CTGGGG-----TCAAG-AC TGACAATCCCATGTAAGGTGTTCTCTGGG 1802  
Qy 573 ArgArgSerArgLeuLysGluProGluLeuGlnSerSer-----Glu 587  
Db 1803 AACCGGCACACCTTAAACCAACATGCTGTGTGGAGCGGCAATGACACCCACATAGAGAG 1862  
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly\*\*\*MetSerLys----- 601  
Db 1863 CGCCTACCCGGGAGCGCGGTGACCCGCGGCGCCAGGCAATATTTCAGAAAATAATGA 1922  
Qy 602 -----HisArgGlyLysSerSerAla 608  
Db 1923 GAACTACATTGAAGTGCCATTGATTTTGTATCTGTGCACAAGAGAGGATTTGCACATGGA 1982  
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628  
Db 1983 TTTTAAATGTGTGTCCTAATAACCTGAGTT--TTCAGACACTACGCACCCAGTCAAGG 2041  
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648  
Db 2042 AAGCCTCTCCAGTTCTCCGAGAC-AAAACCTCACACATGCCCGCCCGTCCCGACACCT 2100  
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666  
Db 2101 GAA-----CTCCTGGGGGAGCGGTCTCAGTCTCTCTCTCCCGCCCAAAACCAAG 2148

RESULT 12  
US-10-282-162-53  
; Sequence 53, Application US/10282162  
; Publication No. US20030143697A1  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING  
; FILE REFERENCE: REG 203-B-US

; CURRENT APPLICATION NUMBER: US/10/282,162  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: 09/787,835  
 ; PRIOR FILING DATE: 1999-09-22  
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045  
 ; PRIOR FILING DATE: 1999-09-22  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 53  
 ; LENGTH: 2754  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-282-162-53

Alignment Scores:  
 Pred. No.: 9,49e-214 Length: 2754  
 Score: 1937.50 Matches: 432  
 Percent Similarity: 62.06% Conservative: 49  
 Best Local Similarity: 55.74% Mismatches: 135  
 Query Match: 52.81% Indels: 161  
 DB: 6 Gaps: 20

US-10-061-727-2 (1-687) x US-10-282-162-53 (1-2754)

QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
 DB 1 ATGGTGCTTCTGTGTGTAGTGAGTCTTACTTTTATGGAACTCTGCAGAGTATGCC 60  
 QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
 DB 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120  
 QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
 DB 121 GAGCAGCTCGCATCAAGTGCCACTCTTTGAACACACTTCTTGAAATTCACCTACAGCACA 180  
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80  
 DB 181 GCCCATTCAGCTGGCTTACTCTGATCTGTTATTTGGACTAGCAGGACCGGGACCTTGAG 240  
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
 DB 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGG 300  
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
 DB 301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACA 360  
 QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
 DB 361 TATTGCAGCAAAAGTTGCAATTTCCCTTGGAGTTGTTCAAAAAGACAGCTGTTCAATTCC 420  
 QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
 DB 421 CCCATGAACCTCCAGTCATATAAAGCTGATATAGAAATATGGCATTTCAGAGGATCACTGT 480  
 QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180  
 DB 481 CCNAATGTAGATGGATATATTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540  
 QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
 DB 541 TGTATATAAATACAGAAATTTAATATGTAATACCCGAGGATGTAAGTCTGAGTTTCCTC 600  
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
 DB 601 ATTGCTTAAATTTCAATAATGGAATTTACACATGTGTTGTGTATACATATCCAGAAAAATGGA 660  
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
 DB 661 CGTAGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720  
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260

DB 721 GTGCCCCCTGTGATCCATTCACTTAATGATCATGTGGTCTATGAGAAAGAACCCAGGACAG 780  
 QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
 DB 781 GAGTACTCATTCCTGTACGGTCTATTTTATGTTTCTGTAGTGGATTCTCGAANTGAGGTT 840  
 QY 281 TrpTrpThrIleAspGlyLysValProAspAspIleThrIleAspValThrIleAsnGlu 300  
 DB 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCCCATTAACGAA 900  
 QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
 DB 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960  
 QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
 DB 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTGTCATGTAGAAAGTGCACAAAGCGAA 1020  
 QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProAlaTyrThrValGluLeu 360  
 DB 1021 GTTCCCAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGCACACA 1080  
 QY 361 -----AlaCysGlyPhe----- 364  
 DB 1081 GGGGCTGCCAAGAGCTGCCGGTTTCGTGGGAGGCATTACAAGCGGAGTTCAGGCTGCAA 1140  
 QY 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384  
 DB 1141 GGGGAGGCTGTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188  
 QY 385 MetValLeuPheTyrArgAlaHisPhe----- 393  
 DB 1189 GCCTCTGACCCCGCCGATCACTGACATGGCATAAAAATGACTCTGTAGAGCGGTC 1248  
 QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412  
 DB 1249 CCAGGAGAAGAAGAGACACGAGTGTGGCCCGAGGCGGTCTGTGTGGCTTCTGCCAGCC 1308  
 QY 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432  
 DB 1309 TTGCAGGAGGACTCTGGCACCCTACGTCTGCACACTAGATAAATGCTTCTTACTGTGACAAA 1368  
 QY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452  
 DB 1369 ATGTCCATTGAGCTCAGAGTTTTTGAG-----AATACA---GAT 1404  
 QY 453 AlaValPheAspPheIleGlnArgSerArgMetIle-----ValVal 467  
 DB 1405 GCTTTCCTGCGTTTCATCTCATACCCGCAAAATTTTAACTTGTCAACCTCTGGGGTATTA 1464  
 QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487  
 DB 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488  
 QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507  
 DB 1489 -----ACCCGTGACAAAACCTGAGTGAAGATTCAATGGTACAA- 1527  
 QY 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527  
 DB 1528 -----GATTCTCTTCTTTGGATAAAGACAAATGAGAAATTTCTTAAGTGTGAGGGGACC 1581  
 QY 528 LysSer----- 529  
 DB 1582 ACTCACTTACTCGTACACGATGTGGCCCTGGAGAGATGCTGGCTATTACCGCTGTGCTGT 1641  
 QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544  
 DB 1642 ACATTTCCCATGAAAGCCAGCAATACACATCACTAGGAGTATTGAGCTACGCATCAAG 1701  
 QY 545 -----ProLeuArgSerLeuSerAlaSer 552  
 DB 552 -----ProLeuArgSerLeuSerAlaSer 552

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Db 1702 AAAAAAAAAAGAGAGACCATTCCTGTGATCATTTCCCCCTCAGACCATATCAGCTTCT 1761
Qy 553 SerGlyTrpAenGluSerCysSerGlnSerAspIleSerLeuAepHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ACTGACAAATCCCATGTAAGGTGTTCTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
Db 1803 AACCGGCACACCCCTTAACACCATGCTGTGTGTGGACGGCCAAATGACACCCACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCTACCGGGAGCGCGTGACCGAGGGGCCACGCCAGGAATATTCAGAAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACCTACATTGAAGTGCATTTGATTTTGTCTGTCTCACAAGAGAGGATTTGCACATGGA 1982
Qy 609 ThrCysArgCysValThrTyrCysGluGlyGluAenHisLeuArgAenLysSerArg 628
Db 1983 TTTTAAATGTGTGTCATATACCTCGAGTT-PTCAGACACATACGCCACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAenGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 -----AAGCCTCTCCACGT--- 2056
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer 668
Db 2057 -----TCTCCGGAGAGTCCAAATACGGTC 2080
Qy 669 AlaLeuAlaLeuHisHisPheThrAspLeuSerAenAsnAsp 683
Db 2081 CGCCATGCC---CATCATGCCACACCTGAGTTCTCTGGGGGGAC 2122
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## RESULT 13

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US-10-282-162-55
; Sequence 55. Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-55
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## Alignment Scores:

Pred. No.:	9.49e-214	Length:	2754
Score:	1937.50	Matches:	432
Percent Similarity:	62.06%	Conservative:	49
Best Local Similarity:	55.74%	Mismatches:	135
Query Match:	52.81%	Indels:	161
DB:	6	Gaps:	20

US-10-061-727-2 (1-687) x US-10-282-162-55 (1-2754)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGATGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
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Db 61 TCAGAACGGCTGCCATGACTGGGAGCTAGACACCATAGAGGCAAAATCCAAGTGTGTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAenTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCACCTCTTTGAACACACTTCTTTGAAATTTCAACTACAGACACA 180
Qy 61 AlaHisSerIaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGTGATTGGACTAGGAGGACCGGAGACCTTTGAG 240
Qy 81 GluProIleAenPheArgLeuProGluAenArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GACCCAAATTAACCTTCGCTCCCGAGAACCGCATTTAGTAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAenAspThrGlyAenTyrThrCysMetLeuArgAenThrThr 120
Db 301 TTCGGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAGNAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAenSer 140
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCAGTGCATAAATCTGATATAGAAATATGGCAATTCAGAGATCATTGT 480
Qy 161 ProAenValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAATGTAGATGATATTTCTTCCAGTGTCAAACCGACTATCACTTGTATATATGGGC 540
Qy 181 CysTyrLysIleGlnAenPheAenAenValIleProGluGlyMetAenLeuSerPheLeu 200
Db 541 TGTATATAAAATACAGAAATTTTAATAATGTAATACCCGAAAGGTATGAATTTGAGTTTCC 600
Qy 201 IleAlaLeuIleSerAenAenGlyAenTyrThrCysValValThrTyrProGluAenGly 220
Db 601 ATTGCCTTTAATTTCAAATATGGAATTTACACATGTGTGTTACATATATCCAGAAATATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAenAla 240
Db 661 CGTACGTTTTCATCTCACAGGACTCTGACTGTAAAGTAGTAGTCTCTCCAAAATAATGCA 720
Qy 241 ValProProValIleHisSerProAenAenHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCTCTGTGATCCATTTCACTAATGATCATGTGTCTATGAGAAAGAACACGAGAGAG 780
Qy 261 GluLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArgAenGluVal 280
Db 781 GAGCTACTCATTCCTCTGACGGTCTATTTTATGTTTCTGATGGATTTCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAenGlu 300
Db 841 TGGTGACCATTTGATGGAATAAAACCTGATGACATCACTATTGATGTCAACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAGAAACAGAAAGATGAACAAAGAACTCAGATTTTGTAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCGTCTGCTAGAGTGTGCAAGGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCAGATACACAGTGACACA 1080
Qy 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAGAAAGCTGCCGGTTCGTGGGAGGCATTACAAGCGGAGGTTTCAGGCTGGAA 1140
Qy 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGGAGCCTGTAGCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188
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Qy	385	MetValLeuPheThrArgAlaHisPhe-----	393
Db	1189	GCCTCTGTGCAGCCCGCATCAACCTGCATGGCATAAATGACTCTGCTAGGACGGTC	1248
Qy	394	--GlyThrAspGluThrIleLeuAspGlyLysGluThrAspIleTyrValSerTyrAla	412
Db	1249	CCAGAGAGAGAGACACGAGATGTGGCCCGACGCGGTCTGTGGCTTCTGCCAGGCC	1308
Qy	413	ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu	432
Db	1309	TTGCAGGAGGACTCTGGCACCTACTGTCACCTACTAGAAATGCTTCTTACTGTGACAAA	1368
Qy	433	PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu	452
Db	1369	ATGTCCATTGAGCTCAGAGTTTGTGAG-----AATACA--GAT	1404
Qy	453	AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal	467
Db	1405	GCITTCCTCGGTTCACTCATACCCCGCAATTTTAACCTTGTCAACCTCTGGGGTATTA	1464
Qy	468	LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal	487
Db	1465	GTATGCCCTGCAC-----CTGAGTGAATTC-----	1488
Qy	488	MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis	507
Db	1489	-----ACCCTGTGACAAACCTGCGTGAAGATTCAATGGTACAAG-----	1527
Qy	508	ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu	527
Db	1528	-----GATTCCTCTCTTTGGATAAGACATGACGAAATTTCTAAGCTGTGAGGGGACC	1581
Qy	528	LysSer-----	529
Db	1582	ACTCACTTACTCGTACAGATGTGGCCCTGGAGATGCTGGCTATTACCCTGTGTCCCTG	1641
Qy	530	-----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu---	544
Db	1642	ACATTGCCCATGAAGGCCAGCAATAACAATCACTAGGAGTATTGAGCTACCGCATCAAG	1701
Qy	545	-----ProLeuArgSerLeuSerAlaSer-----	552
Db	1702	AAAAAAAAGAGAGACCAATTCCTGTGATCATTTCCCTCCCTCAAGACCATATCAGCTTCT	1761
Qy	553	SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAphHisValGlnArg	572
Db	1762	CTGGGG-----TCAAG-ACTGACAATCCCATGTAAAGGTGTTTCTGGG	1802
Qy	573	ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu	587
Db	1803	AACGGGCACACCCTTAACCACTGCTGTGTGGTGGACGGCCAATGACACCCACATAGAG	1862
Qy	588	ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys-----	601
Db	1863	CGCCTACCCGGAGCGCGGTGACCGAGGGGCCACGCGAGGATATTCAGAAATAATGA	1922
Qy	602	-----HisArgGlyLysSerSerAla	608
Db	1923	GAACTACATTGAAGTGCATTTGATTTTGTCTGTGTGACGAGAGGATTTGCACATAGGA	1982
Qy	609	ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg	628
Db	1983	TTTTAAATGTGTGTGCCATATAATCCCTGAGTT-TTCAGACACTACGCACACAGTCAAGG	2041
Qy	629	AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu	648
Db	2042	-----AAGCCTCTCTCCACGT---	2056
Qy	649	SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer	668
Db	2057	-----TCTCGGAGAGTCCAAATACGGTC	2080

Qy	669	AlaLeuAlaLeuHisHisPheThrAspLeuSerAsnAsnAsp	683
Db	2081	CGCCATGCC---CACCATGCCAGCACCTGAGTTCTCGGGGGAC	2122
RESULT 14			
US-10-840-138-23			
; Sequence 23, Application US/10840138			
; Publication No. US20040224893A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Li-Hsien			
; APPLICANT: Lin, Hsin-Chieh			
; APPLICANT: Karow, Margaret			
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat			
; FILE REFERENCE: REG 207A			
; CURRENT APPLICATION NUMBER: US/10/840.138			
; CURRENT FILING DATE: 2004-05-06			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 23			
; LENGTH: 2754			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-840-138-23			
Alignment Scores:			
Pred. No.:		9.49e-214	Length: 2754
Score:		1937.50	Matches: 432
Percent Similarity:		62.06%	Conservative: 49
Best Local Similarity:		55.74%	Mismatches: 135
Query Match:		52.81%	Indels: 161
DB:		8	Gaps: 20
US-10-061-727-2 (1-687) x US-10-840-138-23 (1-2754)			
Qy	1	MetThrLeuLeuTrpCysValValSerLeuTyrrPheTyrrGlyIleuGlu	
Db	1	ATGGTGCTTCTCGTGTGTAGTCACTCTACTTTTATGGAATCCTGCAC	
Qy	21	SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnVa	
Db	61	TCAGAACGCTCGATGACTGGGGACTAGACACCATGAGGCAATCCAGAT	
Qy	41	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAs	
Db	121	GAGCCAGCTGCATCAAGTGCCCACTCTTTGAACACTTCTTGAATTCAA	
Qy	61	AlaHisSerAlaGlyLeuThrLeuIleTrpTyrrThrArgGlnAspArg	
Db	181	GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGCAGACCG	
Qy	81	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAs	
Db	241	GAGCCAAATTAACTTCCGCTCCCCGAGAACCGCATTAGTAGGAGAAAGN	
Qy	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrrThrCysMetLeuAr	
Db	301	TTCCGGCCCCACTCTCTCAATGACACATGGCAACTATACCTGCATGTAAG	
Qy	121	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCy	
Db	361	TATTGTCAGCAAAAGTTGCATTTTCCCTTGGAGTTGTTCAAAAAGACAGCTG	
Qy	141	ProMetLysLeuProValHisLysLeuTyrrIleGluTyrrGlyIleGlnAr	
Db	421	CCCATGAACACTCCCGAGTCATAAATCTGTATAGAAATATGGCATTCAGAG	
Qy	161	ProAsnValAspGlyTyrrPheProSerSerValLysProThrIleThrTrp	
Db	481	CCAAATGTAGATGATATTTTCTTCCAGTGTCAACCGCATATACCTATG	
Qy	181	CysTyrrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu	
Db	541	TGTTATAAATACAGAAATTTTAAATAGTAAATACCCGAAGGTATGAACCTT	



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Qy 201 IleAlaLeuIleSerAsnAsnGlyValThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCTTAATTTCAAATAATGGAAATACACATGTGTGTATACATATCCAGAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTAGGTTTCATCTCACCAGGACTGACTGTAAGGTAGTAGGCTCTCCAAAATAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTAACCTAATGATCATGTGTCTATGAGAAAGAACACGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATCTCCCTGTACGGTCTATTATTAGTTTCTGTAGTGAATCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAGACAGAAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTGCCAAAGCAGCAGGAGTGAGCAGCAAGAGTGCCAGCTCCAGATACACAGTGACACA 1080
Qy 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAAGACTGCCGTTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140
Qy 365 GlyAlaThrValLeuLeuValValIleLeuValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGAGGCTGTAGCCCTGAGGCTGCGGAGGTC-----CCCTACTGTTGTGG 1188
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Db 1189 GCCTCTGTAGCCCCCGCATCAACCTGACATGGCATGATAAAATGACTCTGTAGACGGTC 1248
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
Db 1249 CCAGGAGAAGAAGACAGACCGATGTGGGCCAGGCGTGCTCTGTGGCTTCTGCCAGCC 1308
Qy 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Db 1309 TTGCAGAGGACTCTGGCACTAGCTGTGCACTACTAGAAATGCTTCTTACTGTGACAA 1368
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgSerLeuProGlyGlyAsnThrValGlu 452
Db 1369 ATGTCCATTGAGTCAGATTTTGAG-----AATACA---GAT 1404
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
Db 1405 GCITTCCTGCGGTTCATCTCATACCCGCAAAATTTAACCTTGTCAACCTCTGGGGTATTA 1464
Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
Db 1489 -----ACCCGTGACAAAACCTGAGCGTGAAGATTCAATGGTACAG----- 1527
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTCTTTGGTATAAAGACAATAGAGAAATTTCTTAAGTGTGAGGGGACC 1581
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Qy 528 LysSer----- 529
Db 1582 ACTCATTACTCGTACAGATGTGGCCCTGGAAAGATCTGGCTATTACCGCTGTGTCTCG 1641
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTTCCTCCATGAAGCCAGCAATACAACATCACTAGGAGTATTGAGCTACGATCAAG 1701
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAGAGACCATTCCTGTGTCATATTTCCTCCCTCAAGACCATATCAGTTCT 1761
Qy 553 SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-AC TGACAATCCCATGTAAGGTGTTTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
Db 1803 AACGGGCACACCCCTTAACCAACCATGCTGTGTGGAGCGGCCAATGACACCCACATAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCTACCCGGGAGCGCGCTGACCGAGGGGCCACGCAAGAAATATTTCAGAAAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACATCAATTGAAGTGCCATTGATTTTGTGATCTCTGCACAAAGAGAGGATTTGCACATGA 1982
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAATGTGTGTCTCAATAATACCTGAGTT--TTCAGACACTACGCACACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 -----AAGCCTCTCTCCACGT--- 2056
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer 668
Db 2057 -----TCTCCGGAGAGTCCAAAATACGGTC 2080
Qy 669 AlaLeuAlaLeuHisPheThrAspLeuSerAsnAsnAsp 683
Db 2081 CGCCATGCC---CATATGCCAGCACCTGAGTTCTTGGGGGGAC 2122

RESULT 15
US-10-840-138-25
; Sequence 25, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
; APPLICANT: Lin, Hsin Chieh
; APPLICANT: Karow, Margaret
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840,138
; CURRENT FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-138-25

Alignment Scores:
Pred. No.: 9,49e-214 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: 8 Gaps: 20

US-10-061-727-2 (1-687) x US-10-840-138-25 (1-2754)
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QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
DB 1 ATGGTGCTTCTGTGTGTGTAGTAGTCTCTACTTTTATGGAAATCTCTGCAAAAGTATGCC 60  
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
DB 61 TCAGAACGCTGCGATGACTGGGAGCTAGACACCATGAGGCAAAATCCAAGTGTTCAGAT 120  
QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
DB 121 GAGCCAGCTCGCATCAAGTGCACCTCTTTGAACACCTCTTCAAAATTCAACTACAGACA 180  
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80  
DB 181 GCCCATTCAGCTGGCTTACTCTGATCTGTGTATTTGGACTAGACAGACCGGAGACCTTGA 240  
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
DB 241 GAGCCAAATTAATTCGGCTCCCGAGAACCGCATTTAGTAAGGAGAGATGTGTGTGG 300  
QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
DB 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACA 360  
QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
DB 361 TATTCGAGCAAGTGTGCAATTCCTTGGAGTGTTCAAAAGACAGCTGTTCATTTCC 420  
QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
DB 421 CCCATGAATCCCAAGTGCATAAATCTGATATAGAATATGGCATTCAGAGATCACTGT 480  
QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180  
DB 481 CCAATGTAGATGGATATTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540  
QY 181 CysTyrValIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
DB 541 TGTATAAAATACAGAAATTTAATAATGTAATACCCGAGGTATGAATCTGAGTTTCCTC 600  
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValValTyrProGluAsnGly 220  
DB 601 ATTGCTTTAAATTTCAAAATAGGAATTTACATGTGTGTGTATATCCAGAAATGGA 660  
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
DB 661 CGTAGCTTTCACTCACCAAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720  
QY 241 ValProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
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QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
DB 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGGATCTCGCAATGAGGT 840  
QY 281 TrpTrpThrIleAspGlyLysLysProAspIleThrIleAspValThrIleAsnGlu 300  
DB 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACATTAACGAA 900  
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
DB 901 AGTAAAGTCATAGTAGAACAGAAATGAAACAGAACTCAGATTTTTCAGATCAAGAAA 960  
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
DB 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTCTCATGTAGTAAGTGCACCAAGGCCAA 1020  
QY 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
DB 1021 GTTGCCAAAGCAGCCAAAGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGCACACA 1080

QY 361 -----AlaCysGlyPhe----- 364  
DB 1081 GGGGCTGCCAAGAGCTGCGGTTCGTGGAGGCATTACAGCGGGAGTTTCAGGTGGAA 1140  
QY 365 GlyAlaThrValLeuValIleLeuLeuIleValValTyrHisValTyrTrpLeuGlu 384  
DB 1141 GGGGAGCGCTGTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188  
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QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412  
DB 1249 CCAGGAGAAAGAGACACGAGTGTGGCCCGAGGAGGTCTCTGTGGCTTCGCCAGCC 1308  
QY 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432  
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QY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452  
DB 1369 ATGTCCATTGAGCTCAGAGTTTTCAG-----AATACA---GAT 1404  
QY 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467  
DB 1405 GCTTTCCTGCGTTCATCTCATACCGCAATTTTAACCTTGTCAACCTCTGGGGTATTA 1464  
QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487  
DB 1465 GTATGCCCTGAC-----CTGATGAATTC----- 1488  
QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507  
DB 1489 -----ACCCGTGACAAAACCTGACGTGAAGATTCAATCGTCAAG----- 1527  
QY 508 ProHisProGlyIleLeuGlnLysGluSerValSerPheValSerTrpLysGlyGlu 527  
DB 1528 -----GATTCCTCTTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581  
QY 528 LysSer----- 529  
DB 1582 ACTCACTTACTCGTACAGATGTGCCCTCGGAAGATGTGGCTATTACCGCTGTCTCTG 1641  
QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544  
DB 1642 ACATTTGCCCATGAAGGCCAGCAATACAACATCACTACAGTATTTGAGCTACGCATCAAG 1701  
QY 545 -----ProLeuArgSerLeuSerAlaSer 552  
DB 1702 AAAAAAAGAGAGACCATTCCTGTGATCATTTTCCCTCCCTCAAGACCATATCAGCTTCT 1761  
QY 553 SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572  
DB 1762 CTGGGG-----TCAAG-ACTCACAATCCCATGTAAGGTGTTCTCTGG 1802  
QY 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587  
DB 1803 AACCGGCACACCTTAACCCACCATGCTGTGTGGACGGCCCAATGACACCCACATAGAG 1862  
QY 588 ArgAlaAlaGlySerPro-----ProAlaProGly\*\*\*MetSerLys----- 601  
DB 1863 GGCCTACCGGGGCGCGGTGACCGAGGGGCCAGCCGAGGAATATTTCAGAAAATAATAGA 1922  
QY 602 -----HisArgGlyLysSerSerAla 608  
DB 1923 GAACCTATTGAAGTGCATTGATTTTGTATCTCTGCACAGAGAGGATTTTGCATGGA 1982  
QY 609 ThrCysArgCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628  
DB 1983 TTTTAAATGTGTGTCATATACCTCAGT-TTCAGACACACTACGCCACCAAGTCAAGG 2041  
QY 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGluGlu 648



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 14, 2005, 15:34:05 ; Search time 209 Seconds  
(without alignment)

1611.180 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVVSLYFYGILQSDA.....SALAHHTDLSNNDFYIL 687

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4161359 seqs, 245077644 residues

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10061727/runat\_07122005\_113339\_17291/app\_query.fasta\_1.839  
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10061727@cgn1\_1\_148@runat\_07122005\_113339\_17291  
-NCPU=6 -ICPU=3 -NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARM\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA\_New.\*

1: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1938	52.8	2748	7	US-11-144-987-21
2	1937.5	52.8	2754	7	US-11-144-987-23
3	1937.5	52.8	2754	7	US-11-144-987-25
4	1935	52.7	2703	7	US-11-144-987-9
5	1935	52.7	2709	7	US-11-144-987-11
6	1935	52.7	2709	7	US-11-144-987-13
7	1930	52.6	2733	7	US-11-144-987-1
8	1833	50.0	2703	7	US-11-144-987-3

9	1833	50.0	2709	7	US-11-144-987-5
10	1833	50.0	2709	7	US-11-144-987-7
11	1830	49.9	2754	7	US-11-144-987-17
12	1830	49.9	2754	7	US-11-144-987-19
13	1829	49.9	2748	7	US-11-144-987-15
14	425.5	11.6	2188	6	US-10-995-561-365
15	252	6.9	1197	6	US-10-821-234-731
16	233.5	6.4	3888	6	US-10-995-561-367
17	200	5.5	5178	6	US-10-750-185-48357
18	195.5	5.3	4058	6	US-10-995-561-366
19	148.5	4.0	2943	6	US-10-995-561-437
20	148.5	4.0	14943	6	US-10-995-561-13344
21	148	4.0	23907	7	US-11-186-731-6
22	148	4.0	24120	7	US-11-186-731-4
23	146.5	4.0	54946	6	US-10-995-561-13479
24	135	3.7	1388	6	US-10-750-185-48351
25	134.5	3.7	3283	6	US-10-131-826A-357
26	124	3.4	4017	6	US-10-821-234-770
27	123.5	3.4	26772	6	US-10-995-561-13313
28	123	3.4	14342	6	US-10-821-234-303
29	120	3.3	201	6	US-10-995-561-9887
30	120	3.3	6719	6	US-10-995-561-456
31	119.5	3.3	2867	6	US-10-995-561-357
32	119.5	3.3	3431	6	US-10-995-561-358
33	119.5	3.3	6633	6	US-10-995-561-312
34	119.5	3.3	45038	6	US-10-995-561-13311
35	115.5	3.1	13650	6	US-10-995-561-155
36	115.5	3.1	13711	6	US-10-995-561-154
37	115.5	3.1	14194	6	US-10-995-561-153
38	114.5	3.1	5130	7	US-11-135-855-12
39	114.5	3.1	5158	7	US-11-135-855-13
40	111	3.0	4053	6	US-10-131-826A-351
41	109.5	3.0	5050	6	US-10-995-561-388
42	109.5	3.0	5200	6	US-10-995-561-387
43	109.5	3.0	5694	6	US-10-821-234-783
44	109.5	3.0	5832	6	US-10-995-561-389
45	109.5	3.0	7741	7	US-11-000-463-14

#### ALIGNMENTS

##### RESULT 1

US-11-144-987-21  
; Sequence 21, Application US/11144987  
; Publication No. US20050272655A1  
; GENERAL INFORMATION:  
; APPLICANT: Mellis, Scott  
; APPLICANT: Karow, Margaret  
; APPLICANT: Yancopoulos, George  
; APPLICANT: Papadopoulos, Joanne  
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease  
; FILE REFERENCE: REG 2090A  
; CURRENT APPLICATION NUMBER: US/11/144,987  
; CURRENT FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: 60/577,023  
; PRIOR FILING DATE: 2004-06-04  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 2748  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-144-987-21

Alignment Scores:			
Pred. No.:	3.1e-184	Length:	2748
Score:	1938.00	Matches:	432
Percent Similarity:	63.42%	Conservative:	50
Best Local Similarity:	56.84%	Mismatches:	141
Query Match:	52.82%	Indels:	140
DB:	7	Gaps:	19

US-10-061-727-2 (1-687) x US-11-144-987-21 (1-2748)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20  
Dbb 1 ATGGTGGCTTCCTGGTGTAGTGAGTCTCTACATTTTATGGAATCCTGCAAGTGTATGCC 60  
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40  
Dbb 61 TCAGAACGCTCGGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT 120  
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60  
Dbb 121 GAGCAGCTGCATCAAGTGCCTCTTTTGAAACATCTTGAATTCACACTACAGACACA 180  
Qy 61 AlahisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80  
Dbb 181 GCCCATTTAGCTGGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGAGCTTTGAG 240  
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100  
Dbb 241 GAGCAATTAATCTCCGCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 300  
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120  
Dbb 301 TTCCGGCCCACTCTCCTCAATGACACTGGCACTATACCTGCAATGTTAAGGAACACTACA 360  
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140  
Dbb 361 TATTGCAAGCAAGTGTCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATCC 420  
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160  
Dbb 421 CCCATGAACCTCCAGTGTCATAAATCTGTATAGATATGGCAATTCAGAGGATCACTTGT 480  
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180  
Dbb 481 CCAATGTAGATGATATTTCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC 540  
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200  
Dbb 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAAAGTATGAATTTGAGTTTCTC 600  
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220  
Dbb 601 ATTGCCCTTAATTTCAAATAATAGGAATTTACATATGTTGTATACATATCCAGAAAAATGGA 660  
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240  
Dbb 661 CGTAGCTTTCACTCTACCAAGGACTCTGACTGTAAAGTAGTAGGCCTCTCCAAAAATGCA 720  
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260  
Dbb 721 GTGCCCTCTGTATCCATTTACCTTAATGATCATGTGTGTTATGAGAAAGAACCCAGGAGAG 780  
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280  
Dbb 781 GAGCTACTCAATTCCTGTAGCGGTCTATTTAGTTTCTGATGATTTCTCGCAATGAGGTT 840  
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300  
Dbb 841 TGGTGGACCAATGATGAAAAAACCCTGATGACATCACTATTGATGTCAACATTAACGAA 900  
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320  
Dbb 901 AGTATAGTCTAGTAGTAGAAGAGATGAAACAGAACTCAGATTTTGTAGCATCAAGAA 960  
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340  
Dbb 961 GTTACCTCTGAGGATCTCAAGCCGAGCTATGTCTGTCATGCTAGAAAGTGCAGAAAGCGAA 1020  
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360  
Dbb 1021 GTTGCCAAACAGCCCAAGGTGAAGAGAAAGTCCAGCTCCAGATACACAGTGCACACA 1080

Qy 361 -----AlaCysGlyPhe----- 364  
Dbb 1081 GGGGCTGCCAAGAGCTGCCGGTTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140  
Qy 365 GlyAlaThrValLeuLeuValIleLeuIleValTyrHisValTyrTrpLeuGlu 384  
Dbb 1141 GGGAGGCTGTAGCCCTGAGGTGCCCCAGGTG-----CCCTACTGTTGTGG 1188  
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393  
Dbb 1189 GCCTCTGTAGCCCCCGCATCAACCTGACATGCGCATATAAATGACTCTGTAGACCGGTC 1248  
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412  
Dbb 1249 CCAGGAGAAAGAGACACCGATGTGGCCCGAGACGGTGTCTGTGGCTTCTGCCAGCC 1308  
Qy 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432  
Dbb 1309 TTGCAGGAGGACTCTGGCACTACGTCTGCACCTAGAGAAATGCTTCTTACTGTGACAAA 1368  
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452  
Dbb 1369 ATGTCCATTGAGCTCAGAGTTTGTAG-----AATACA---GAT 1404  
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467  
Dbb 1405 GCTTCTCTGCGGTTCATCTCATACCCGCAAAATTTTAACTTGTCAACCTCTGGGGTATTA 1464  
Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487  
Dbb 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488  
Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507  
Dbb 1489 -----ACCGTGCAAACTGACGTGAAGATTCATGGTACAAG----- 1527  
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527  
Dbb 1528 -----GATTCTCTCTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581  
Qy 528 LysSer----- 529  
Dbb 1582 ACTCACTTACTCTGACAGATGTGGCCCTGGAAAGATGTGGCTATTACCCGCTGTGCTGTG 1641  
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544  
Dbb 1642 ACATTTGCCCATGAAGCCAGCAATACACATCACTAGGAGTATTGAGCTACGCATCAAG 1701  
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552  
Dbb 1702 AAAAAAAGAGAGAGACCATTCCTGTGATCATTTCCCTCCCTCAAGACCATATCAGCTTCT 1761  
Qy 553 SerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572  
Dbb 1762 CTGGGG-----TCAAG-ACGTGACAATCCCATGTAAGTGTTCCTGGG 1802  
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587  
Dbb 1803 AACCGGCACACCTTAAACCCACCATGCTGTGTGGAGCGGCCAATGACACCCACATAGAGAG 1862  
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly\*\*\*MetSerLys----- 601  
Dbb 1863 CGCTACCCGGAGGCGCGGTGACCGGGCCAGCAGGAATATTCAGAAAAATAATGA 1922  
Qy 602 -----HisArgGlyLysSerSerAla 608  
Dbb 1923 GAACATACATTGAAGTGCCCATTTGATTTTGTCTCTGTCAAGAGAGGATTTTGACATGGA 1982  
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628  
Dbb 1983 TTTTAAATGTGTGTCCATAATACCTCTGAGTT-TTCAGACACTTACCGCACACAGTCAAGG 2041  
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648

481	Db	CCAAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGCATATCACTTGGTATATGGGC	540
181	Qy	CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu	200
541	Db	TGTTATAAATAACAGAAATTTTAAATATGTAATACCGAAGGTATGAACCTTGAGTTTCCTC	600
201	Qy	IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly	220
601	Db	ATTGCCTTAATTTCAAATTAATGAAATTAACACATGTGTTGTTACATATCCAGAAAATGGA	660
221	Qy	ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	240
661	Db	CGTACCGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA	720
241	Qy	ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	260
721	Db	GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTATATGAGAAAGAACCCAGAGAG	780
261	Qy	GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	280
781	Db	GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGTGATTCTCGCAATGAGGTT	840
281	Qy	TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu	300
841	Db	TGCTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCCACCATTAACGAA	900
301	Qy	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	320
901	Db	AGTATTAAGTCATAGTAGAACAGAAAGATGAACAAAGAACTCAGATTTTGGACATCAAGAAA	960
321	Qy	ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaAlaArgSerAlaLysGlyGlu	340
961	Db	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAAGTGCCAAAGCGCAA	1020
341	Qy	ValAlaLysAlaAlaLysValLysGlnLysValProAlaLysValThrValGluLeu	360
1021	Db	GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCACAGTCCAAAGATACACAGTGCACACA	1080
361	Qy	-----AlaCysGlyPhe-----	364
1081	Db	GGGGCTGCCAAGAGCTGCCGGTTTCTGGGAGGCATTACAAGCGGAGTTCAGCGTGGAA	1140
365	Qy	GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu	384
1141	Db	GGGGAGCCCTGAGCCCTGAGGTGCCCCAGGTG-----CCCTACTGTTGTGG	1188
385	Qy	MetValLeuPheTyrArgAlaHisPhe-----	393
1189	Db	GCCTCTGTGAGCCCCCGCATCAACCTGCATGCGCATGAAAAATGACTCTGCTAGGACGGTC	1248
394	Qy	---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla	412
1249	Db	CAGGAGAAAGAGACACGGATGTGGCCGACGGTGTCTCTGTGGCTTCTGCCAGCC	1308
413	Qy	ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu	432
1309	Db	TTGCGAGGAGCTCTGGCACCTACGCTCGCATCTAGAAATGCTTCTTACTGTGACAAA	1368
433	Qy	PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu	452
1369	Db	ATGTCCATTGAGCTCAGAGTTTTTGAG-----AATACA--GAT	1404
453	Qy	AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal	467
1405	Db	GCTTTCTCCCGTTTCATCTCATACCCGCAAAATTTAAACCTTGTCAACCTCTGGGGGTATTA	1464
468	Qy	LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal	487
1465	Db	GTATGCCCTGAC-----CTGAGTGAATTC-----	1488
488	Qy	MetCysGlnAsnSerIleAlaThrLysLysIleValValGluTyrArgProLeuGluHis	507

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Db 1489 -----ACCGGTGACAAABACGCTGACGCTGAAGATTCAATGGTACAAG----- 1527
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTTCTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581
Qy 528 LysSer----- 529
Db 1582 ACTCACTTACTGCTACAGATGTGGCCCTGGAAGATGTGGCTATTACCGCTGTGCTGTG 1641
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACAITGGCCATGAAGGCGAGCAATACACATCACTAGGAGTATTGACCTACGATCAAG 1701
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAGAGACCATTCCTGTGATCATTTCCGCCCTCAAGACCATATCAGCTTCT 1761
Qy 553 SerGlyTrpAenGluSerCysSerSerGlnSerAspLysSerLeuAspHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ActGACAATCCCATGTAAAGTGTGTTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
Db 1803 AACCGGCACACCTTAACCAACCATGCTGTGTGGAGCGGCCAATGACACCCACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly**MetSerLys----- 601
Db 1863 CGCTACTCCGGAGGCGCGGTGACCGAGGGGCCACGCCAGGAATATTGAGAAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAATCACTGAAGTGCAATGATGATTTTGTGTCCTGTCACAGAGAGGATTTGCACATGGA 1982
Qy 609 ThrCysArgCysCysValThrTrpCysGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAAATGTGTGTCATAATACCTGAGTT-TTCAGACACTACGACACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAenGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 -----AAGCCTCTCTCCACGT--- 2056
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer 668
Db 2057 -----TCTCCGGAGAGTCCAAATACGGTC 2080
Qy 669 AlaLeuAlaLeuHisHisPheThrAspLeuSerAsnAsnAsp 683
Db 2081 CGCCATGCC---CATCATGCCACGCTGAGTTCTCTGGGGGAC 2122

RESULT 3
US-11-144-987-25
; Sequence 25, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-25
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Alignment Scores:
Pred. No.: 3,49e-184 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: 7 20
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US-10-061-727-2 (1-687) x US-11-144-987-25 (1-2754)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyPheTyTrpGlyIleLeuGlnSerAspAla 20
Db 1 ATGTGTCTTCTGTGTGTGTAGTGAGTCTCTACTTTTATGGAATTCCTGCAAGTGTGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTCGCATGACTGGGACATAGACCCATGAGGCAATCCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTySerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCACACTCTTTGAAACACTTCTTGAATTCACACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuLeuTrpTyTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGCGCTTACTCTGTATTTGGACTAGGACGAGCCGGGACCTTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTAGTAAGAGAGAAAGATGTGCTGTGG 300
Qy 101 PheArgProThrLeuLeuAenAspThrGlyAsnTyThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCATCTCTCTCAATGACACTGCGCAACTATACCTGCGCATGTTAAGGAACACTACA 360
Qy 121 TrpCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTGGCATTTCCCTTGGAAAGTTGTTCAAAAAGACACGCTGTTTCAAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyIleGluTyTrpIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCAGTGCATAAATCTATATAGATATGCGCATTCAGAGAGATCATTGT 480
Qy 161 ProAsnValAspGlyTyTrpPheProSerSerValLysProThrIleThrTrpTyMetGly 180
Db 481 CCAAAATGTAGATGGATATTTTCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyTrpLysIleGlnAsnPheAenAsnValIleProGluGlyMetAenLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAAGGTATGAACCTTGAGTTTCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyThrCysValValThrTyTrpProGluAsnGly 220
Db 601 ATTGCCCTTAATTTCAATAATGAAATTAACACATGTGTGTTACATATATCCAGAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTTCTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyTrpGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGTATTCATTACCTAATGATCATGTGTGTCTATGAGAAAAGAACACGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyTrpPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGATCTCTCGCAATGAGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGACCATTTGATGAAAAAACCCTGATGACATCACTATTGATGTGTCACCAATTAAGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 320
Db 901 AGTATTAAGTCATAGTAGAACAGAGATGAACAAAGAACTCAGATTTTGGACATCAAGAA 960
```

```
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
|||
DB 961 GTTACTCTGAGATCTCAAGCGCAGCTATGTCGTCTCATGCTAGAAAGTCCAAAGCGCAA 1020
QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
|||
DB 1021 GTTGCCAAAGCAGCCAAAGTGAAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGCCACACA 1080
QY 361 -----AlaCysGlyPhe----- 364
|||
DB 1081 GGGGCTGCCAAGCTGCCGGTTCTCGGAGGCATTACAAGCGGAGTTCCAGCGTCGAA 1140
QY 365 GlyAlaThrValLeuValValIleLeuIleValValTyrHisValTyrTripleGlu 384
|||
DB 1141 GGGGAGCCTGTAGCCTGAGCTGAGTGCGCCCGCAGGTG-----CCCTACTGTGTGTGG 1188
QY 385 MetValLeuPheTyrArgAlaHisPhe----- 393
|||
DB 1189 GCCTCTGTGAGCCCGCATCAACCTGACATGGCATAAATAGACTCTGTAGGACGGTC 1248
QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
|||
DB 1249 CCAGGAGAAAGACAGACCGATGTGGCCCGCAGGCGGTCTCTGTGGCTTCTGCGCACC 1308
QY 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
|||
DB 1309 TTGCAGGAGGACTGTGGCACCCTGCTGCTGCTAGTAATGCTTCTTACTGTGACAAA 1368
QY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
|||
DB 1369 ATGTCATTGAGCTCAGATTTTCAG-----AATACA---GAT 1404
QY 453 AlaValPheAspPheIleGlnArgSerArgMetIle-----ValVal 467
|||
DB 1405 GCTTTCCTGCGCTTCATCTACCCGCAAAATTTTAACCTTTGTCAACCTCTGGGGTATTA 1464
QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
|||
DB 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
|||
DB 1489 -----ACCGTGACAAACTGACGTGAAGATTCATGGTACAAG----- 1527
QY 508 ProHisProGlyIleLeuGlnLysGluSerValSerPheValSerTripleGlyGlu 527
|||
DB 1528 -----GATTCTCTCTTTTGGATAAAGACAAATGAGAAATTTCTAAGTGTGAGGGGACC 1581
QY 528 LysSer----- 529
DB 1582 ACTCACTTACTGTACAGATGTGGCCCTGGAAAGATGCTGATTAACCGGTGTGTCGTG 1641
QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
DB 1642 ACATTTGCCCATGAGGCCAGCAATACACATCACTAGGAGTATTGAGCTACGCATCAAG 1701
QY 545 -----ProLeuArgSerLeuSerAlaSer 552
DB 1702 AAAAAAAAAAAGAGACCATTCCTGTGATCATTTCCCCCTCAAGACCATATCAGCTTCT 1761
QY 553 SerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
DB 1762 CTGGGG-----TCAAG-ACTGACAATCCCATGTAAAGGTGTTTCTGGG 1802
QY 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
DB 1803 AACCGGCACACCTTTAACCAACCATGCTGTGTGGAGCGGCCCAATGACACCCACATAGAG 1862
QY 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
DB 1863 GCGCTACCCGGGAGGCCGCGTGACCGGAGGGGCCACGCCAGGAAATATTTCAGAAATAATGA 1922
```

```
QY 602 -----HisArgGlyLysSerSerAla 608
DB 1923 GAACACATATTGAAGTGCATTGATTTTGTATCTCTGCACAGAGAGATTTCACATGGA 1982
QY 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
DB 1983 TTTTAAATGTGTGTCTCCATAATACCTCAGTTTTCAGACACACTACGCACACAGTCAAGG 2041
QY 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
DB 2042 -----AAGCCTCTCCACGT--- 2056
QY 649 SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer 668
DB 2057 -----TCTCCGGAGAGTCCAAATACGGTC 2080
QY 669 AlaLeuAlaLeuHisHisPheThrAspLeuSerAsnAsnAsp 683
DB 2081 CGCCATGCC---CACCATGCCAGCACCTGAGTTCTCTGGGGGGAC 2122
```

## RESULT 4

```
US-11-144-987-9
; Sequence 9, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-9
```

```
Alignment Scores:
Pred. No.: 6,06e-184 Length: 2703
Score: 1935.00 Matches: 358
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.74% Indels: 0
DB: 7 Gaps: 0
```

US-10-061-727-2 (1-687) x US-11-144-987-9 (1-2703)

```
QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
|||
DB 1 ATGGTGCTTCTGTGTGTGTAGTGTAGTCTCTACTTTTATGCAATCTTCGAAAGTATGCC 60
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTCGCATGACTGGGGACTACACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT 120
QY 41 GluProAlaArgIleLysCysPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 121 GAGCAGCTCCGATCAAGTGGCCCACTCTTTGAACACTTCTTGAATTCCTTCACTACAGCACA 180
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCATTCAGTGGCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 240
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
DB 241 GAGCAATTAATCTTCCGCTCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGTGTGG 300
```



```
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCACTCTCCCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGACAGCAAGTTGCATTTCCCTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACCTCCCGAGTGCATAAACTGTATATAGATATATGCAATTCAGAGGATCACTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCCTTCCAGTGTCAAAACCGACTATCACTGTGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAGGTATGAACCTTGAGTTTCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTATACATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCACTCAACAGAGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTCTATGNGAAGAACACAGAGAG 780
Qy 261 GluLeuLeuLeProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATTCCTCTGACGGTCTATTTTAGTATTTCTGATGGATTCCTCAATAGAGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCACTGATGAAAAAACCCTGATGACATCACTATTGATGTACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGACAGAGAGATGAACAAGAACTCAGATTTTGACATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTCATGTAGAAGTGCCTCAAGGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAAGTGCCAGCTCCAGATACACAGTGGAA 1077
```

## RESULT 5

```
US-11-144-987-11
; Sequence 11, Application US/111144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIOR FILING DATE: 2005-06-03
; PRIOR FILING DATE: 2005-06-03
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
```

## US-11-144-987-11

```
Alignment Scores:
Pred. No.: 6,08e-184 Length: 2709
Score: 1935.00 Matches: 358
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.74% Indels: 0
DB: 7 Gaps: 0
```

## US-10-061-727-2 (1-687) x US-11-144-987-11 (1-2709)

```
Qy 1 MetThrLeuLeuTyrPheValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGTGTATGCC 60
Qy 21 SerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGCCATGACTGAGTGGGACTAGACACCATGAGGCAATCCCAAGTGTGTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCACACTCTTTGAAACACTTCTTGAAATTTCAACTACAGCACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTGGACTAGGCGAGGACCGGACCTTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
Db 241 GAGCCAAATTAACCTTCGCCCTCCCGAGAACCGCATTAGTAGAGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGACAGCAAGTTGCATTTCCCTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCATGAAACTCCAGTGCATATAAATGTATATAGATATGTCATTCAGAGATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCCTTCCAGTGTCAAACCGACTATCACTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAGGTATGAACCTTCCTCAAGTTTCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTATACATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCACTCAACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTCTATGAGAAAAGAACACAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATTCCTCTGACGGTCTATTTTAGTATTTCTGATGGATTCCTCAATAGAGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCACTGATGAAAAAACCCTGATGACATCACTATTGATGTACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
```

```

Db      901 AGTATAAGTCATAGTAGAACAAGAGTGAACCAAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy      321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db      961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAAGTCCCAAGAGCGGAA 1020
Qy      341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db      1021 GTTGCCAAAGCAGCCAGGTAAGGAGCAGAAAAGTGCCAGCTCCCAAGATACACAGTGGAA 1077

RESULT 6
US-11-144-987-13
; Sequence 13, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2050A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-13

Alignment Scores:
Pred. No.: 6,08e-184 Length: 2709
Score: 1935.00 Matches: 358
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.74% Indels: 0
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-13 (1-2709)
Qy      1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db      1 ATGGTGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
Qy      21 SerGluArgCysAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db      61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTGAAGAT 120
Qy      41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db      121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTTTGAACACTCTTTGAACACTTACAGCACA 180
Qy      61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db      181 GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGCTAGCTAGCAGGACCGGACCTTGAG 240
Qy      81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db      241 GAGCCCAATTACTTCGCGCTCCCGAGAACCGCATTTAGGAGAAAGATGTGCTGTGG 300
Qy      101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db      301 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATCTGATGCTTTAAGGAACACTACA 360
Qy      121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
Db      361 TATTTCAGCAAGATTGCATTTCCCTTGAAGTGTGTTCAAAAGACAGCTGTTTCAATTCC 420
Qy      141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160

```

```

Db      421 CCCATGAACCTCCAGTGTCATAAACTGTATATAGAAATATGCAATTCAGAGGATCACTTGT 480
Qy      161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180
Db      481 CCAATGTAGATGATATTTTCCCTCCAGTGTCAAAACGACTATACACTTGGTATATGGGC 540
Qy      181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db      541 TGTATATAAATACAGAAATTTTAATAATGTAATACCCGAAAGGTATGAACCTTGAGTTTCCTC 600
Qy      201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db      601 ATTGCCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTATACATATCCAGAAAATGGA 660
Qy      221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db      661 CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy      241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db      721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTGTCTATGAGAAAGAACCCAGGAGAG 780
Qy      261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db      781 GAGCTACTCATCTCCCTGTACGGTCTATTTTATGTTTCTGTATGATGATTCGCAATGAGGTT 840
Qy      281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db      841 TGGTGGACCAATGATGAAAAAAACCTGATGACATCACTATTGTATGTCCACATTAAACGAA 900
Qy      301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db      901 AGTATAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy      321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db      961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAAGTCCCAAGAGCGGAA 1020
Qy      341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db      1021 GTTGCCAAAGCAGCCAGGTAAGGAGCAGAAAAGTGCCAGCTCCCAAGATACACAGTGGAA 1077

RESULT 7
US-11-144-987-1
; Sequence 1, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2050A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-1

Alignment Scores:
Pred. No.: 1.97e-183 Length: 2733
Score: 1930.00 Matches: 357
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.60% Indels: 0
DB: 7 Gaps: 0

```

US-10-061-727-2 (1-687) x US-11-144-987-1 (1-2733)

```
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCTGTGTGTAGTGAGTCTCTACITTTATGGAATCCTGCAAGGTGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTCGCATGATGCGGACTAGACACCATGAGGCAAAATCCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAenTyrSerThr 60
Db 121 GAGCCAGCTCCATCAAGTGCCTCTTTGAAACACTCTTTGAAATTCACACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTTGAGTGGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGGAG 240
Qy 81 GluProIleAenPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACCTTCCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAenThrThr 120
Db 301 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAGCAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAATCCAGTGCAATAAATCTATATAGAAATATGGCAATTCAGAGGATCACATTGT 480
Qy 161 ProAenValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAANTGTAGATGATATTTTCTTCCAGTGTCAACCGACTATCACTTGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAenPheAsnValIleProGluGlyMetAenLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAGGTATGAATTTGAGTTTCTCTC 600
Qy 201 IleAlaLeuIleSerAenAsnGlyAsnTyrThrCysValValThrTyrProGluAenGly 220
Db 601 ATTGCCCTTAAATTTCAAAATAATGGAATAATACACATGTGTGTTTACATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAenAla 240
Db 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATCAGAAAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAenGluVal 280
Db 781 GAGCTACTCAATTCCTGTAGCGGTCTAATTTAGTTTTCGTATGGAATCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAenGlu 300
Db 841 TGTGGGCCCAATTTATGAAAAAACCCTGATGACATCACTATTGATGTACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAGAAGACAGAAATGAAACAAGAACTCAGATTTTGGACCATCAAGAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCCGAGCTATGTCTGTATGCTAGAAAGTGCAGAAAGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrVal 358
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Db 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAAAGTCCAGCTCCAGATACACAGTG 1074

## RESULT 8

US-11-144-987-3  
; Sequence 3, Application US/11144987  
; Publication No. US20050272655A1  
; GENERAL INFORMATION:  
; APPLICANT: Mellis, Scott  
; APPLICANT: Karow, Margaret  
; APPLICANT: Yancopoulos, George  
; APPLICANT: Papadopoulos, Joanne  
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease  
; FILE REFERENCE: REG 2090A  
; CURRENT APPLICATION NUMBER: US/11/144,987  
; PRIOR FILING DATE: 2005-06-03  
; PRIOR FILING DATE: 2004-06-04  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2703  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-11-144-987-3

Alignment Scores:  
Pred. No.: 1,15e-173 Length: 2703  
Score: 1833.00 Matches: 339  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 49.96% Indels: 0  
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-3 (1-2703)

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Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 997 TCAGAACGCTGCGCATCAAGTGCCTCTTTGAAACACTCTCTTGAATTCACACTACAGACA 1056
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAenTyrSerThr 60
Db 1057 GAGCCAGCTCGCATCAAGTGCCTCTTTGAAACACTCTCTTGAATTCACACTACAGACA 1116
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 1117 GCCCATTTGAGTGGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGGAG 1176
Qy 81 GluProIleAenPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 1177 GAGCCAAATTAACCTTCCCGCTCCCGAGAACCCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 1236
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAenThrThr 120
Db 1237 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCAATGTTAAGGAACACTACA 1296
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 1297 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 1356
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 1357 CCCATGAATCCAGTGCAATAAATCTATATAGAAATATGGCAATTCAGAGGATCACATTGT 1416
Qy 161 ProAenValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 1417 CCAANTGTAGATGATATTTTCTTCCAGTGTCAAAACCGCACTATCACTTGTATATGGGC 1476
Qy 181 CysTyrLysIleGlnAenPheAenAenValIleProGluGlyMetAenLeuSerPheLeu 200
Db 1477 TGTATATAAATAACAGAAATTTAATAATGTAATACCCGAGAGGTATGAATTTGAGTTTCTCTC 1536
Qy 201 IleAlaLeuIleSerAenAenGlyAenTyrThrCysValValThrTyrProGluAenGly 220
```

Db 1537 ATTGCCTTAATTTCAAATAATCGAAATATACACATGTTGTTGTATACATATCCAGAAAATGGA 1596

Qy 221 ArgThrPheHisLeuThrArgThrLeuThrVallysValValGlySerProlysAsnAla 240

Db 1597 CGTAGCTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATAATGCA 1656

Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260

Db 1657 GTGCCCTCTGTATCCATTCACATTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716

Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280

Db 1717 GAGCTACTCATTTCCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTCGCAATGAGGTT 1776

Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300

Db 1777 TGGTGGACCATTTGATGGAAAAAACTGATGACATCACTATTATGATGTACCATTAAACGAA 1836

Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320

Db 1837 AGTATAAGTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 1896

Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340

Db 1897 GTTACCTCTGAGGATCTCAAGCCGAGCTATGTCTGTCATGCTAGAAAGTGCACAAAGCGAA 1956

Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359

Db 1957 GTTGCACCAAGCCAGGTGAAGCAGAAAAGTGCAGCTCCAAAGATACACAGTGGAA 2013

RESULT 9

US-11-144-987-5

; Sequence 5, Application US/11144987

; Publication No. US20050272655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; FILE REFERENCE: REG 2090A

; CURRENT APPLICATION NUMBER: US/11/144,987

; CURRENT FILING DATE: 2005-06-03

; PRIOR APPLICATION NUMBER: 60/577,023

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-144-987-5

Alignment Scores:

Pred. No.: 1,15e-173 Length: 2709

Score: 1833.00 Matches: 339

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 49.96% Indels: 0

DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-5 (1-2709)

Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40

Db 997 TCAGAACCTCGATGACTGGGACTAGACACCATGAGGCAAACTCAAGTGTGTTGAAGAT 1056

Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60

Db 1057 GAGCCAGCTCGCATCAAGTGCCACTCTTTGAACACTTCTTGAATTCACATACAGACA 1116

Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80

Db 1117 GCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACATAGGACGAGACCGGACCTTGAG 1176

Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100

Db 1177 GAGCAATTAATTTCCGCTCTCCCGAGAACCGCATTTAGTAGGAAAGATGTGTGTGG 1236

Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120

Db 1237 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAACAACACTACA 1296

Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140

Db 1297 TATTGCAAGAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 1356

Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160

Db 1357 CCCATGAACCTCCAGTGCATAACTGTATATAGNATATGGCATTCAGAGNATCACTGT 1416

Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180

Db 1417 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACCTGGTATATGGGC 1476

Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200

Db 1477 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGAGTTTCC 1536

Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220

Db 1537 ATTGCCTTAATTTCAAATTAATGGAAATTTACACATGTGTTGTACATATCCAGAAAATGGA 1596

Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProlysAsnAla 240

Db 1597 CGTAGCTTTCATCTCACCAGGACTCTGACTCTAAAGGTAGTAGGCTCTCCAAAAAATGCA 1656

Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260

Db 1657 GTGCCCTCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAAGAACCCAGGAG 1716

Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280

Db 1717 GAGTACTCATCTCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTCCTCGCAATGAGGTT 1776

Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300

Db 1777 TGGTGGACCATTTGATGGAAAAAACTGATGACATCACTATTGATGTCCACATTAACGAA 1836

Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320

Db 1837 AGTATAAGTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTTCAGCATCAAGAAA 1896

Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340

Db 1897 GTTACCTCTGAGGATCTCAAGCCGAGCTATGTCTGTCATGCTAGAAAGTGCACAAAGCGAA 1956

Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359

Db 1957 GTTGCACCAAGCCAGGTGAAGCAGAAAAGTGCAGCTCCAAAGATACACAGTGGAA 2013

RESULT 10

US-11-144-987-7

; Sequence 7, Application US/11144987

; Publication No. US20050272655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; FILE REFERENCE: REG 2090A

; CURRENT APPLICATION NUMBER: US/11/144,987

; CURRENT FILING DATE: 2005-06-03

; PRIOR APPLICATION NUMBER: 60/577,023

; PRIOR FILING DATE: 2004-06-04

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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-7

Alignment Scores:
Pred. No.:      1,15e-173      Length:      2709
Score:          1833.00        Matches:      339
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      49.96%      Indels:        0
DB:              7           Gaps:          0

US-10-061-727-2 (1-687) x US-11-144-987-7 (1-2709)

Qy  21  SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp  40
Db  997 TCAGAACGCTCGAGTACTGGGGACTAGACACCAATGAGGCAAAATCCAAAGTGTTTGAAGAT 1056

Qy  41  GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr  60
Db  1057 GAGCCAGCTCGCATCAAGTGCCTCTTTGAACACTTCTTGAATTTCAACTACAGACACA 1116

Qy  61  AlahisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArgAspLeuGlu  80
Db  1117 GCCCATTTTCAGTGGCTTACTCTGATCTGGTATTTGGACTAGGACGACCGGACCTTGGAG 1176

Qy  81  GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp  100
Db  1177 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAAGGAGAAAGATGTCTGTGG 1236

Qy  101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr  120
Db  1237 TTCGGGCCACTCTCTCCATGACACTGGCACTATACCTGCATGTTAAGGAACACTACA 1296

Qy  121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer  140
Db  1297 TATTGCGAGCAAGTTGCATTTCCCTTGGAAAGTTTCCAAAAGACAGCTGTTTCAATTC 1356

Qy  141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys  160
Db  1357 CCCATGAACATCCCAAGTGCATAAACTGTATAGAAATATGCAATGCGCATTCAGAGATCATTGT 1416

Qy  161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly  180
Db  1417 CCAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCATTGGTATATGGGC 1476

Qy  181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu  200
Db  1477 TGTATATAAATACAGAAATTTTAATAATAGTAATACCCGAAGGTATGAACTTGAGTTTCCTC 1536

Qy  201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly  220
Db  1537 ATTGCCCTTAATTTCAAATAATAGGAATATACACATGTGTGTATACATATCCAGAAAAATGGA 1596

Qy  221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla  240
Db  1597 CGTAGCTTTCATCTCACCGAGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 1656

Qy  241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu  260
Db  1657 GTGCCCCCTGTGATCCATTACCTTAATGATGATGTGCTGTATGAGAAAGAACCCAGGAGAG 1716

Qy  261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal  280
Db  1717 GAGTACTCATCTCCCTGTGACGGTCTATTTAGTTTTCGTGATGATTCCTGCAATGAGGTT 1776

Qy  281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu  300
Db  1777 TGGTGGACCATTCATGGAAAAAACCCTGATGACATCACTATTGATGTACCATTTACGAA 1836
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Qy  301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys  320
Db  1837 AGTATAAGTTCATAGTAAACAGAAAGATGAAACAAAGAACTCAGATTTTTCAGCATCAAGAAA 1896

Qy  321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu  340
Db  1897 GTTACCTCTCAGGATCTCAAGCCGACGCTATGTCTCATGTAGAAAGTGCACAAAGGCGAA 1956

Qy  341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProAspGlyThrValGlu  359
Db  1957 GTTGCCTCAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCCAGATACACAGTGGAA 2013

RESULT 11
US-11-144-987-17
; Sequence 17, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-17

Alignment Scores:
Pred. No.:      2,37e-173      Length:      2754
Score:          1830.00        Matches:      340
Percent Similarity: 97.99%    Conservative: 1
Best Local Similarity: 97.70% Mismatches:      7
Query Match:      49.88%      Indels:        0
DB:              7           Gaps:          0

US-10-061-727-2 (1-687) x US-11-144-987-17 (1-2754)

Qy  18  SerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnVal  37
Db  1036 TCACAGTTTTCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTG 1095

Qy  38  PheGluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsn  57
Db  1096 TTTGAAGATGAGCAGCTGCTGATCAAGTGCCTCTTTTGAACACTTCTTTGAAATTCAC 1155

Qy  58  TyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArg  77
Db  1156 TACAGACACAGCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTTGGACTAGGACGACCGG 1215

Qy  78  AspLeuGluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAsp  97
Db  1216 GACCTTGAGGAGGCAATTAACCTTCCGCTCCCGAGAACCCGCAATTAGTAGGAGAAAGAT 1275

Qy  98  ValLeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg  117
Db  1276 GTGCTGTGGTTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTCATGTGTTAAGG 1335

Qy  118 AsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys  137
Db  1336 AACACTACATATATTGACAGCAAGTTGCATTTCCCTTGGAAAGTTGTTTCAAAAAGACAGCTGT 1395

Qy  138 PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArg  157
Db  1396 TTCATTTCCCCCATGAAACTCCCGATGCAATAAACTGTATATAGANTATGCGCATTCAGAGG 1455
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QY 158 ileThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
Db 1456 ATCACTGTGCCAAATGTAGATGATATTTTCTCCAGTGTCACACCGACTATCACTTGG 1515
QY 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu 197
Db 1516 TATATGGGCTGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAACITG 1575
QY 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro 217
Db 1576 AGTTTCTCATTTGCCCTTAATTTCAAAATATGGAATTTACACATGTTGTTTACATATCCA 1635
QY 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerPro 237
Db 1636 GAAATATGGACGTACGTTTCATCTCACCAGACTCTGACTGTAAAGGTAGTAGGCTCTCCA 1695
QY 238 LysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluLysGlu 257
Db 1696 AAAAATGGCAGTGCCTCCCTGTGATCCATTCCACCTAATGATCATGTGTTCTATGAGAAAGAA 1755
QY 258 ProGlyGluGluLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArg 277
Db 1756 CCAGGAGAGAGCTACTCAATCCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTTCTCGC 1815
QY 278 AsnGluValTyrTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThr 297
Db 1816 ATAGAGTTTGTGTGACCATTCATGGAAAAAACCTGTATGATCATCTATTGATGTACCC 1875
QY 298 IleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSer 317
Db 1876 ATTAACGAAAGTATAAGTCATAGTAGAACAGAAAGTAAACAAAGAACTCAGATTTTGAGC 1935
QY 318 IleLysLysValThrSerGluAspLeuLysValLysGlnLysValProAlaProArgTyrThr 357
Db 1936 ATCAAGAAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAAGTGCC 1995
QY 358 ValGluLeuAlaCysGlyPheGly 365
Db 2056 GTGTCGGAGAGTCCAAATACGGT 2079

RESULT 12
US-11-144-987-19
; Sequence 19, Application US/11144987
; Publication NO. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Mellis, Scott
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-19

Alignment Scores:
Pred. No.: 2,37e-173 Length: 2754
Score: 1830.00 Matches: 340
Percent Similarity: 97.99% Conservative: 1
Best Local Similarity: 97.70% Mismatches: 7
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Query Match: 49.88% Indels: 0
DB: 7 Gaps: 0
US-10-061-727-2 (1-687) x US-11-144-987-19 (1-2754)
QY 18 SerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnVal 37
Db 1036 TCCAGCTTCTCAGAACGCTGCGATGACTGGGACTAGACACCATCAGGCAAAATCCAAAGTG 1095
QY 38 PheGluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsn 57
Db 1096 TTTGAAGATGAGCCAGCTCGCATCAAGTGCCCACTCTTTTGAACACTTCTTTGAAATTTCAAC 1155
QY 58 TyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArg 77
Db 1156 TACAGCAGACCCCATTCAGCTGGCTTACTCTGATCTGTATTTGACATAGGACAGCCGG 1215
QY 78 AspLeuGluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAsp 97
Db 1216 GACCTTGAGGAGCCAAATTAACCTTCGCCCTCCCGAGAACCGCATTTAGTAAGGAGAAAGAT 1275
QY 98 ValLeuTrpPheArgProThrIleLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
Db 1276 GTGCTGTGGTTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTGTAAGG 1335
QY 118 AsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys 137
Db 1336 AACACTACATATTCGACGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGACTGT 1395
QY 138 PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArg 157
Db 1396 TTCAATTTCCCAATGAAACTCCCAAGTGCATAAATAGATATAGATAATAGGCATTCAGAGG 1455
QY 158 IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
Db 1456 ATCACTTGTCCAAATGTAGATGSGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGG 1515
QY 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu 197
Db 1516 TATATGGCTGTTATATAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAACITG 1575
QY 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro 217
Db 1576 AGTTTCTCTCATTTGCCCTTAATTTCAAAATATAGAAATACACATGTGTTGTTTACATATCCA 1635
QY 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerPro 237
Db 1636 GAAATATGGACGTACGTTTTCATCTCACCAGGACTCTGACTGTAAAGGTATAGGCTCTCCA 1695
QY 238 LysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluLysGlu 257
Db 1696 AAAATGCAAGTGCCTCCCTCTGTGATCCATTCACATATGATCATGTGTTCTATGAGAAAGAA 1755
QY 258 ProGlyGluGluLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArg 277
Db 1756 CCAGGAGAGGAGCTACTCAATCCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTTCTCGC 1815
QY 278 AsnGluValTyrTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThr 297
Db 1816 AATGAGGTTTGGTGGACCAATTTGATGGAAAAAACCTGATGACATCACTATTGATGTACCC 1875
QY 298 IleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSer 317
Db 1876 ATTAACGAAAGTATAAGTCATAGTAGAACAGAAAGTAAACAAAGAACTCAGATTTTGAGC 1935
QY 318 IleLysLysValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAla 337
Db 1936 ATCAAGAAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAAGTGCC 1995
QY 338 LysGlyGluValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThr 357
Db 1996 AAAGCGAAGTTGCAAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCAAAGATACACA 2055
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Qy 358 ValGluLeuAlaCysGlyPheGly 365
Db 2056 GTGTCGGAGAGTGCAAAATACGGT 2079

RESULT 13
US-11-144-987-15
; Sequence 15, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Papadopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-15

Alignment Scores:
Pred. No.: 2,98e-173 Length: 2748
Score: 1829.00 Matches: 339
Percent Similarity: 99.41% Conservative: 0
Best Local Similarity: 99.41% Mismatches: 2
Query Match: 49.85% Indels: 0
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-15 (1-2748)

Qy 18 SerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnVal 37
Db 1036 TCCAGCTTCTCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTG 1095

Qy 38 PheGluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsn 57
Db 1096 TTGGAAGTGAAGCAGCTCGCATCAAGTCCCACTCTTTGAACACTCTTTGAAATTCAC 1155

Qy 58 TyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTrpThrArgGlnAspArg 77
Db 1156 TACAGCACAGCCATTCCAGCTGGCTTACTCTGATCTGGTATTGGACTAGCAGGACCG 1215

Qy 78 AspleuGluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAsp 97
Db 1216 GACCTTGAGGAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGAT 1275

Qy 98 ValLeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
Db 1276 GTGCTGTGGTTCGGCCCACTCTCTCAATGACACTGGCACTATACCTCATGTTAAGG 1335

Qy 118 AsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys 137
Db 1336 AACACTACATATTGCAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAGACAGCTGT 1395

Qy 138 PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArg 157
Db 1396 TTCAATTTCCCCCAATGAACCTCCAGTGTCATAAACTGTATATAGAAATATGCGCATTCAGAG 1455

Qy 158 IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
Db 1456 ATCACTGTCCAAATGTAGATGAAATTTTCCTTCAGTGTCAACCGCATCATCCTTGG 1515

Qy 178 TyrMetGlyCysTyrIleGlnAsnPheAsnValIleProGluGlyMetAsnLeu 197
Db 1516 TATATGGCTGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAAGGTATGAACCTTG 1575
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Qy 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro 217
Db 1576 AGTTTCTCATTCGCTTAATTTCAAATAATAGAAATTTACACATGTTGTTTACATATCCA 1635

Qy 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerPro 237
Db 1636 GAAATATGGAGCTAGCTTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCA 1695

Qy 238 LysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluLysGlu 257
Db 1696 AAAATATGCAGTGGCCCTGTGATCCATTACCTAATCATCATGTGGTCTATGAGAAAGAA 1755

Qy 258 ProGlyGluGluLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArg 277
Db 1756 CCAGGAGAGAGCTACTCATTCCTGTACGCTCTATTTAGTTTCTGTGATGATTCGCG 1815

Qy 278 AsnGluValTrpTrpThrIleAspGlyLysLeuProAspAspIleThrIleAspValThr 297
Db 1816 AATGAGTTTGGTGGACCATTTGATGAAAAAACCTGATGACATCATTTGATGTCCACC 1875

Qy 298 IleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSer 317
Db 1876 ATTAACGAAAGTATAAGTCATAGTACAGACAGAGATGAACACAGAACTCAGATTTTCAGC 1935

Qy 318 IleLysLysValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAla 337
Db 1936 ATCAAGAAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCATGTAGAAAGTGCC 1995

Qy 338 LysGlyGluValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThr 357
Db 1996 AAAGGCGAAGTTGCCAAAGCAGCCAAAGGTGAAGAGAAAGTCCAGCTCCCAAGATACACA 2055

Qy 358 Val 358
Db 2056 GTG 2058

RESULT 14
US-10-995-561-365
; Sequence 365, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 2188
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-365

Alignment Scores:
Pred. No.: 5,46e-32 Length: 2188
Score: 425.50 Matches: 152
Percent Similarity: 39.42% Conservative: 92
Best Local Similarity: 24.56% Mismatches: 231
Query Match: 11.60% Indels: 145
DB: 6 Gaps: 22

US-10-061-727-2 (1-687) x US-10-995-561-365 (1-2188)

Qy 27 TrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluProAlaArgIleLys 46
Db 306 TGGGGGCTG-----GAAATAGAGGCTTTAATTTGTAAGA 338

Qy 47 CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeu 66
Db 339 TGTCTCT-----AGACAAAGAAACCTAGTTAC 365
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QY 67 ThrLeuIleTyrTrpThrArgGlnAspArgLeuGluGluProIleAsnPheArg 86
|||...
366 ACCGTGGATGGTATATCTACCAACAACAAAGATATT-----CCCACTCAGGAAGA 419
QY 87 LeuProGluAsnArgIleSerLysGluLysAspValLeuTyrPheArgProThrLeuLeu 106
|||...
420 -----AATCGTGTGTTGCCTCAGGCCAACCTCTGAAAGTTCTACCAAGCTGMAGT 470
QY 107 AsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSerLysValala 126
|||...
471 GVTGATCTGGTATTATACCTGTATTGTCAAGTCCACACATTCAATAGGACTGGATAT 530
QY 127 PheProLeuGluValValGlnLysAspSerCysPheAsnSerProMetLysLeuProVal 146
|||...
531 GCGAATGTCACCATATATAAACAACATCAGATTGCAATGTTCCAGAT----- 578
QY 147 HisLysLeuTyrIleGluTyrGlyle-----GlnArgIleThr 159
|||...
579 -----TATTGATGATTCAACAGTATCTGGATCAGAAAAAATTCCAAAATTTAT 629
QY 160 CysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMet 179
|||...
630 TGTCTCATCATGACCTCTAC-----AACTGGACAGCACCTCTTGAGTGGTTAAG 680
QY 180 GlyCysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPhe 199
|||...
681 AATTGTCAGGCTCTTCAAGGATCAAG-----TACAGGGCGCACAAAGTCATT 728
QY 200 LeuIle-----AlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyr 216
|||...
729 TTGGTCATTGATAATGTGACTGAGGACRCAGGTGATTACACCTGTAATTTATACAC 788
QY 217 ProGluAsnGlyArgThrPheHisLeu-----ThrArgThrLeuThrValVal 233
|||...
789 AATGAAATGGAGCCAATTATAGTGTGACGGCCAGGTCCTTCCAGGTCAAGGTTTGG 848
QY 233 -----ValGly----- 233
849 TGTGAGAGTTCGCAAAATTAAGAGAGCTTAATCTTTAGTAATCTATCTGGATTCAA 908
QY 234 -----ValGly----- 235
909 ARTYTAATGAGAGGCTTTGTGATGATATCTATGTTGATACATAAATGTTGTCAGTGT 968
QY 236 -----SerProLysAsn 239
969 TTTAATCTTTGTTGCAATFACCTTTCAACATCATCAATGGCCTTGAATGAGCAAGGCTTT- 1027
QY 240 AlaValProValIleHisSerProAsnAspHisValValTyrGluLysGluProGly 259
|||...
1028 TCTCTGTTCCGTAATCGAGCCCTCGCAAAAATGAATAAGAAAGTGAATTTGGA 1087
QY 260 GluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGlu 279
|||...
1088 AAAAAGCGCAAACTAACTTGCTCTGCTTTTGGAAAAGGCACTCAGTCTCTGGCTGCC 1147
QY 280 ValTrpTrpThrIleAspGlyLysLysProAspAsp-----IleThrIle 294
|||...
1148 GTCTCTGTGGCAGCTTAATAGGAACAAAAATTTACAGACTTTGGTGAACCAAGAAATTCACAA 1207
QY 295 AspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGln 314
|||...
1208 GGGGAAGGGCAAAATCAAGTTTCAAGCAATGGCTGGCT-----TGCTAGACATG 1258
QY 315 IleLeuSerIleLysLysValThrSerGluAspLeuLysArgSerTyrValCysHisAla 334
|||...
1259 GTTTTAAGAATAGCTGAYGTGAAGGAAGAGGATTTATTGCTGCAGTACGACTGTCTGGCC 1318
QY 335 ArgSerAlaLysGlyGluValAlaLysAlaLysValLysGlnLysValProAlaPro 354
|||...
1319 CTGAATTTGCGCTTGTGAGAAGGCACACCGTAAGTAAAGTAAAGGAAAAATCCAAATTGAT 1378
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QY 355 Arg-----TyrThrValGluLeuAlaCysGlyPheGlyAlaThrValLeuLeuVal 371
|||...
1379 CATCATGACTACTGATCAATAATTCAGATATGT-----AGTGTATTATTATGCTAATC 1432
QY 372 ValIleLeuIleValValTyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAla 391
|||...
1433 AATGCTCTGGTTATCATCTCTAAATAATGTTCTGGATTGAGGCCACTCTCTCTGGAGAGAC 1492
QY 392 HisPheGlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyr 411
|||...
1493 ATAGCTAAACCTTCAAGACTAGGAATGATGAAAGCTCTATGATGCTTATGTTCTCTAC 1552
QY 412 AlaArgAsn-----AlaGluGluGluGluPheValLeuLeu 423
|||...
1553 CCACGGAACCTACAAATCCAGTACAGATGGGCCAGTCGTGTAGACACTTTGTTCCACGAG 1612
QY 424 ThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePheAspArgAla 443
|||...
1613 ATTCTGCTGATGTTCTTGAATAATAATGTGGCTATACCTTATGCACTTATGGGAGAGAT 1672
QY 444 SerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArgSerArgArg 463
|||...
1673 ATGCTACTGAGAGATGTAGTCACTCACTGGAACCAACATACGAAAGAGAGCGG 1732
QY 464 MetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPhe 483
|||...
1733 CACATTTTCATCTGACCCCTCAGATCACTCACAAYAGGAGTTGGC---TACGARGCAG 1789
QY 484 LysLeuGlyValMetCys-----GlnAsnSerIleAlaThrLysLeuIleValVal 500
|||...
1790 GAGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1843
QY 501 GluTyrArgProLeu-----GluHisProHisProGlyIle 512
|||...
1844 GAGATGAGGCTGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 1903
QY 513 LeuGlnLeuLysGluSerValSerPheValSerTyrLysGlyGlu-----LysSer 529
|||...
1904 MRGCATCTTATGAAGTACAGGGGACCATCAAGTGGAGGGAGGACCATTCGCCATWATAA 1963
QY 530 LysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSer 548
|||...
1964 AGGTCCCTGAAATTCYAAATTCCTGGAAGCACGTGAGGTACCAAAATGCTGTGCCAAGC 2020

RESULT 15
US-10-821-234-731
; Sequence 731, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 731
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-731

Alignment Scores:
Pred. No.: 6,43e-15 Length: 1197
Score: 252.00 Matches: 79
Percent Similarity: 38.94% Conservative: 53
Best Local Similarity: 23.30% Mismatches: 146
Query Match: 6.87% Indels: 62
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 7, 2005, 13:26:36 ; Search time 26 Seconds  
(without alignments)  
2184.546 Million cell updates/sec

Title: US-10-061-727-2  
Perfect score: 3669  
Sequence: 1 MTLWCVVSLFYGILOSDA.....SALAHHTDLSNNDFYIL 687

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2586	70.5	570	US-08-991-944-2	Sequence 2, Appli
2	2586	70.5	570	US-09-173-151A-36	Sequence 36, Appl
3	2586	70.5	570	US-09-949-016-6184	Sequence 6184, Ap
4	2586	70.5	591	US-09-949-016-11319	Sequence 11319, A
5	2327.5	63.4	570	US-08-991-944-4	Sequence 4, Appli
6	2327.5	63.4	570	US-09-173-151A-21	Sequence 21, Appl
7	1937.5	52.8	915	US-10-282-162-52	Sequence 52, Appl
8	1937.5	52.8	917	US-10-282-162-54	Sequence 54, Appl
9	1937.5	52.8	917	US-10-282-162-56	Sequence 56, Appl
10	1935	52.7	900	US-10-282-162-40	Sequence 40, Appl
11	1935	52.7	902	US-10-282-162-42	Sequence 42, Appl
12	1935	52.7	902	US-10-282-162-44	Sequence 44, Appl
13	1930	52.6	910	US-09-313-942-28	Sequence 28, Appl
14	1930	52.6	910	US-10-282-162-28	Sequence 28, Appl
15	1933	50.0	900	US-10-282-162-34	Sequence 34, Appl
16	1833	50.0	902	US-10-282-162-36	Sequence 36, Appl
17	1833	50.0	902	US-10-282-162-38	Sequence 38, Appl
18	1830	49.9	917	US-10-282-162-48	Sequence 48, Appl
19	1830	49.9	917	US-10-282-162-50	Sequence 50, Appl
20	1829	49.9	915	US-10-282-162-46	Sequence 46, Appl
21	825	22.5	686	US-09-173-151A-4	Sequence 4, Appli
22	800	21.8	579	US-09-173-151A-2	Sequence 2, Appli
23	762.5	20.8	668	US-09-173-151A-35	Sequence 35, Appl
24	528	14.4	541	US-08-604-333-2	Sequence 2, Appli
25	528	14.4	541	US-09-110-618-2	Sequence 2, Appl
26	528	14.4	541	US-09-173-151A-28	Sequence 28, Appl
27	528	14.4	541	US-09-578-178-2	Sequence 2, Appli

28	528	14.4	541	2	US-09-577-806-2	Sequence 2, Appli
29	528	14.4	541	2	US-09-621-502-4	Sequence 4, Appli
30	528	14.4	541	2	US-09-949-002-360	Sequence 360, App
31	528	14.4	545	2	US-09-949-002-489	Sequence 489, App
32	520	14.2	521	2	US-08-996-338-20	Sequence 20, Appl
33	520	14.2	521	2	US-09-556-972-20	Sequence 20, Appl
34	496	13.5	555	2	US-09-173-151A-32	Sequence 32, Appl
35	484.5	13.2	576	1	US-07-821-716-4	Sequence 4, Appli
36	484.5	13.2	576	1	US-08-381-603-4	Sequence 4, Appli
37	484.5	13.2	576	1	US-08-924-376-4	Sequence 4, Appli
38	484.5	13.2	576	2	US-08-685-212-4	Sequence 4, Appli
39	484.5	13.2	576	2	US-09-173-151A-30	Sequence 30, Appl
40	484.5	13.2	576	2	US-08-466-932A-4	Sequence 4, Appli
41	484.5	13.2	576	4	PCT-US94-02414-4	Sequence 4, Appli
42	484.5	13.2	576	4	PCT-US96-08899-4	Sequence 4, Appli
43	479	13.1	537	1	US-08-604-333-4	Sequence 4, Appli
44	479	13.1	537	2	US-09-110-618-4	Sequence 4, Appli
45	479	13.1	537	2	US-09-173-151A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-08-991-944-2  
; Sequence 2, Application US/08991944  
; Patent No. 6280955  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Zhaodan  
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,  
; TITLE OF INVENTION: Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94010  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,944  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 343-4341  
; TELEFAX: (650) 343-4342  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 570 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-991-944-2

Query Match 70.5%; Score 2586; DB 2; Length 570;  
Best Local Similarity 85.3%; Pred. No. 7.8e-244;  
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;  
Oy 1 MTLWCVVSLFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLEHFLKFNYST 60  
Db 1 MTLWCVVSLFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLEHFLKFNYST 60  
Oy 61 AHSAGLTLIYWTYQDRDLDEEPINFRPLPENRISKEKDVLPFRPTLLNDTGYTCLNRWT 120

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Db 61 AHSAGLTLIWTWTRQDRDLPEEPINRPLPENRISKEKOVLMWFRPTLLNDTNGYTCMLRNTT 120
Qy 121 YCSKVAFFLEVVQKDCSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPPTITWYMG 180
Db 121 YCSKVAFFLEVVQKDCSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAKVKQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAKVKQKVPAPRYTVEL 360
Qy 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFPGTDETLIDGKEYDIYVSYARNAEBEEF 420
Db 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFPGTDETLIDGKEYDIYVSYARNAEBEEF 420
Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDIORSRRMIVLVSPDYVTEKSISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDIORSRRMIVLVSPDYVTEKSISM 480
Qy 481 LEFLKGVMCQNSIATK----LIVVEYRPLEHPHFGILQLKES---VSFVSWKGEKSKHSG 533
Db 481 LELKAGL---ENMASRGNINVLQYKAVKETK--VKELKRAKTVLTVIKWKEKSKYPQ 535
Qy 534 SKFWKALRLALPLRLSLASGWNESCSSQSDI 565
Db 536 GRFWKQLQVAMPVKSPRRSSDDEQGLSYSSL 567
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## RESULT 2

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US-09-173-151A-36
; Sequence 36, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173.151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-173-151A-36
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Query Match 70.5%; Score 2586; DB 2; Length 570;

Best Local Similarity 85.3%; Pred. No. 7.9e-244;

Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

Qy 1 MTLWCVVSIFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEHFLKFNYST 60

Db 1 MTLWCVVSIFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEHFLKFNYST 60

Qy 61 AHSAGLTLIWTWTRQDRDLPEEPINRPLPENRISKEKOVLMWFRPTLLNDTNGYTCMLRNTT 120

Db 61 AHSAGLTLIWTWTRQDRDLPEEPINRPLPENRISKEKOVLMWFRPTLLNDTNGYTCMLRNTT 120

Qy 121 YCSKVAFFLEVVQKDCSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPPTITWYMG 180

Db 121 YCSKVAFFLEVVQKDCSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPPTITWYMG 180

Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240

Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240

Qy 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300

Db 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300

Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAKVKQKVPAPRYTVEL 360

Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAKVKQKVPAPRYTVEL 360

Qy 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFPGTDETLIDGKEYDIYVSYARNAEBEEF 420

Db 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFPGTDETLIDGKEYDIYVSYARNAEBEEF 420

Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDIORSRRMIVLVSPDYVTEKSISM 480

Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDIORSRRMIVLVSPDYVTEKSISM 480

Qy 481 LEFLKGVMCQNSIATK----LIVVEYRPLEHPHFGILQLKES---VSFVSWKGEKSKHSG 533

Db 481 LELKAGL---ENMASRGNINVLQYKAVKETK--VKELKRAKTVLTVIKWKEKSKYPQ 535

Qy 534 SKFWKALRLALPLRLSLASGWNESCSSQSDI 565

Db 536 GRFWKQLQVAMPVKSPRRSSDDEQGLSYSSL 567

## RESULT 3

US-09-949-016-6184

; Sequence 6184, Application US/09949016

```
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6184
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6184

Query Match          70.5%; Score 2586; DB 2; Length 570;
Best Local Similarity 85.3%; Pred. No. 7.8e-244;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDPARIKCPLFEHFLKFNYST 60
Db 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDPARIKCPLFEHFLKFNYST 60
QY 61 AHSAGLTLIWYTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLTLIWYTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTT 120
QY 121 YCSKVAFLVQKDSFNSPMKLPVHKLYIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Db 121 YCSKVAFLVQKDSFNSPMKLPVHKLYIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
QY 181 CYKIQNFNNVIEPEGNNLSFLIALISNNGNYTCVVTYPENGRFTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIEPEGNNLSFLIALISNNGNYTCVVTYPENGRFTFHLTRTLTKVVGSPKNA 240
QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
QY 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVPAPRYTVEL 360
QY 361 ACGGATVLLVILVYVHVWLEWVLFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 420
Db 361 ACGGATVLLVILVYVHVWLEWVLFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 420
QY 421 VLLTRGLVLENEFGYKLCIFDRDSLPGGIVTDETLSPFKSRRLVLSPNVLTQGTQAL 480
Db 421 VLLTRGLVLENEFGYKLCIFDRDSLPGGIVTDETLSPFKSRRLVLSPNVLTQGTQAL 480
QY 481 LEFKLGVMCQNSIATK----LIVVEYRPLEHPHPIQLQKES---VSFVSWKGEKSKHSG 533
Db 481 LEFKLGVMCQNSIATK----LIVVEYRPLEHPHPIQLQKES---VSFVSWKGEKSKHSG 533
QY 534 SKFWKALRALPLRLSLASSGWNESCSCSSQSDI 565
Db 534 SKFWKALRALPLRLSLASSGWNESCSCSSQSDI 565
QY 536 GRFWKQLOVAMPVKKSPRRSSDEQGLSYSSL 567
Db 536 GRFWKQLOVAMPVKKSPRRSSDEQGLSYSSL 567
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```
RESULT 4
US-09-949-016-11319
; Sequence 11319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```

```
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11319
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11319
```

```
Query Match          70.5%; Score 2586; DB 2; Length 591;
Best Local Similarity 85.3%; Pred. No. 8.3e-244;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDPARIKCPLFEHFLKFNYST 60
Db 22 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDPARIKCPLFEHFLKFNYST 81
QY 61 AHSAGLTLIWYTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTT 120
Db 82 AHSAGLTLIWYTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNVTCMLRNTT 141
QY 121 YCSKVAFLVQKDSFNSPMKLPVHKLYIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Db 142 YCSKVAFLVQKDSFNSPMKLPVHKLYIEYGIQRTICPNVDGYFPSSVKPTITWYMG 201
QY 181 CYKIQNFNNVIEPEGNNLSFLIALISNNGNYTCVVTYPENGRFTFHLTRTLTKVVGSPKNA 240
Db 202 CYKIQNFNNVIEPEGNNLSFLIALISNNGNYTCVVTYPENGRFTFHLTRTLTKVVGSPKNA 261
QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
Db 262 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 321
QY 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVPAPRYTVEL 360
Db 322 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVPAPRYTVEL 381
QY 361 ACGGATVLLVILVYVHVWLEWVLFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 420
Db 382 ACGGATVLLVILVYVHVWLEWVLFYRAHFGTDETLIDGKEYDIYVSVARNABEEF 441
QY 421 VLLTRGLVLENEFGYKLCIFDRDSLPGGIVTDETLSPFKSRRLVLSPNVLTQGTQAL 501
Db 442 VLLTRGLVLENEFGYKLCIFDRDSLPGGIVTDETLSPFKSRRLVLSPNVLTQGTQAL 501
QY 481 LEFKLGVMCQNSIATK----LIVVEYRPLEHPHPIQLQKES---VSFVSWKGEKSKHSG 533
Db 502 LELKAGL---ENMASRGNINVLQYKAVKETK--VKELKRAKTVLTVIKWKGESKYPQ 556
QY 534 SKFWKALRALPLRLSLASSGWNESCSCSSQSDI 565
Db 557 GRFWKQLOVAMPVKKSPRRSSDEQGLSYSSL 588
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RESULT 5
US-08-991-944-4
; Sequence 4, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
; Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
```



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Oy 61 AHSAGTLIYWTRQDRDLEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGTLIYWTRQDRDLEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Oy 121 YCSKVAFFLEVQKDSFCNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Db 121 YCSKVAFFLEVQKDSFCNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Oy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240
Oy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 CTEIVDFHNVLPEGMNLSFFPLVSNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240
Oy 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Db 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Oy 361 ACAGFATVLLVVLIVVYVHVMVLFYRAHFGTDETLIDGKEVDIYVSARNABEEF 420
Db 361 ACAGFATVLLVVLIVVYVHVMVLFYRAHFGTDETLIDGKEVDIYVSARNABEEF 420
Oy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGNGTVEAVDFIORSRRMIVLSPDVVTEKSISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGNGTVEAVDFIORSRRMIVLSPDVVTEKSISM 480
Oy 481 LEFLGLVNCQSIATK----LIVVEYRPLEHPHGLQLKES---VSFVSWKGEKSKHSG 533
Db 481 LELKAGL---ENMASRGNINVLQYKAVKDMK--VKELKRAKTVLTVIKWGEKSKYPQ 535
Oy 534 SKFWKALRLALPLRLSLSSAGSNES 558
Db 536 GRPMKQLQVAMPVK---SPRWSSN 557
```

## RESULT 7

```
US-10-282-162-52
; Sequence 52, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282.162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-52
```

```
Query Match 52.8%; Score 1937.5; DB 2; Length 915;
Best Local Similarity 80.9%; Pred. No. 5.2e-180;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;
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Oy 1 MTLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Db 1 MVLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Oy 61 AHSAGTLIYWTRQDRDLEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGTLIYWTRQDRDLEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
```

```
Oy 121 YCSKVAFFLEVQKDSFCNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Db 121 YCSKVAFFLEVQKDSFCNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Oy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240
Oy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Oy 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Db 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Oy 361 ----ACGF-----GATVLLVVLIVVYVHVMVLFYRAHF----- 393
Db 361 GAARSCFRGRHRYKREBPGEVLRCPQV----PYWLWASVSPRINLTWHKNDARSATV 416
Oy 394 -GTDETIL---DG-----KEYDIYVSARNABEEFVLLTLRGVLEN 431
Db 417 PGEETRMAODGALWLLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466
```

## RESULT 8

```
US-10-282-162-54
; Sequence 54, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282.162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-54
```

```
Query Match 52.8%; Score 1937.5; DB 2; Length 917;
Best Local Similarity 80.9%; Pred. No. 5.3e-180;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;
```

```
Oy 1 MTLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Db 1 MVLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Oy 61 AHSAGTLIYWTRQDRDLEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGTLIYWTRQDRDLEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Oy 121 YCSKVAFFLEVQKDSFCNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Db 121 YCSKVAFFLEVQKDSFCNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
Oy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVGSPKNA 240
Oy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Oy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
```



Db 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360  
Qy 361 -----ACGF-----GATVLLVVLIVVHVHVLVLEMLVLYRAHF----- 393  
Db 361 GAARSCRFRGRHYKREFRLEGEVALRCPOV-----PYWLWASVSPRINLTWHKNDARSATV 416  
Qy 394 -GTDETL-----DG-----KEYDIYVSVARNAEEEFVLLTLRGVLEN 431  
Db 417 PGBEETRMWAQDGAALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 9  
US-10-282-162-56  
; Sequence 56, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 56  
; LENGTH: 917  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-282-162-56

Query Match 52.8%; Score 1937, 5; DB 2; Length 917;  
Best Local Similarity 80.9%; Pred. No. 5.3e-180;  
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHLKFNYS 60  
Db 1 MVLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHLKFNYS 60  
Qy 61 AHSAGTLIYWYTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120  
Db 61 AHSAGTLIYWYTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120  
Qy 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQITCPNVDGYPSSVKPTITWYMG 180  
Db 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQITCPNVDGYPSSVKPTITWYMG 180  
Qy 181 CYKIQNFNNVPIPEGMNLFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240  
Db 181 CYKIQNFNNVPIPEGMNLFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240  
Qy 241 VPPVHSPNDHVYKEPGEELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300  
Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300  
Qy 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVEL 360  
Db 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360  
Qy 361 -----ACGF-----GATVLLVVLIVVHVHVLVLEMLVLYRAHF----- 393  
Db 361 GAARSCRFRGRHYKREFRLEGEVALRCPOV-----PYWLWASVSPRINLTWHKNDARSATV 416  
Qy 394 -GTDETL-----DG-----KEYDIYVSVARNAEEEFVLLTLRGVLEN 431  
Db 417 PGBEETRMWAQDGAALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 10

US-10-282-162-40  
; Sequence 40, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 40  
; LENGTH: 900  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-282-162-40

Query Match 52.7%; Score 1935; DB 2; Length 900;  
Best Local Similarity 99.7%; Pred. No. 9e-180;  
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHLKFNYS 60  
Db 1 MVLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHLKFNYS 60  
Qy 61 AHSAGTLIYWYTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120  
Db 61 AHSAGTLIYWYTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120  
Qy 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQITCPNVDGYPSSVKPTITWYMG 180  
Db 121 YCSKVAFPLEVQKDSFCNSPMKLPVHKLYIEYGIQITCPNVDGYPSSVKPTITWYMG 180  
Qy 181 CYKIQNFNNVPIPEGMNLFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240  
Db 181 CYKIQNFNNVPIPEGMNLFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240  
Qy 241 VPPVHSPNDHVYKEPGEELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300  
Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300  
Qy 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVE 359  
Db 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVE 359

RESULT 11  
US-10-282-162-42  
; Sequence 42, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 902  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-282-162-42

Query Match 52.7%; Score 1935; DB 2; Length 902;  
 Best Local Similarity 99.7%; Pred. No. 9e-180;  
 Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST 60  
 DB 1 MVLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGLTLLIWTYTRQDRDLLEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120  
 DB 61 AHSAGLTLLIWTYTRQDRDLLEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120

QY 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180  
 DB 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180

QY 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240  
 DB 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300  
 DB 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAVKQKVPAPRYTVE 359  
 DB 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAVKQKVPAPRYTVE 359

RESULT 12  
 US-10-282-162-44  
 ; Sequence 44, Application US/10282162  
 ; Patent No. 6927044  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
 ; FILE REFERENCE: REG 203-B-US  
 ; CURRENT APPLICATION NUMBER: US/10/282,162  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: 09/787,835  
 ; PRIOR FILING DATE: 1999-09-22  
 ; PRIOR FILING DATE: 1999-09-22  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 44  
 ; LENGTH: 902  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-282-162-44

Query Match 52.7%; Score 1935; DB 2; Length 902;  
 Best Local Similarity 99.7%; Pred. No. 9e-180;  
 Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST 60  
 DB 1 MVLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGLTLLIWTYTRQDRDLLEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120  
 DB 61 AHSAGLTLLIWTYTRQDRDLLEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120

QY 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180  
 DB 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180

QY 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240  
 DB 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300  
 DB 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAVKQKVPAPRYTVE 359  
 DB 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAVKQKVPAPRYTVE 359

RESULT 13  
 US-09-313-942-28  
 ; Sequence 28, Application US/09313942  
 ; Patent No. 6472179  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
 ; FILE REFERENCE: REG 203-A  
 ; CURRENT FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: 09/313,942  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: 60/101,858  
 ; PRIOR FILING DATE: 1998-09-25  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 28  
 ; LENGTH: 910  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-313-942-28

Query Match 52.6%; Score 1930; DB 2; Length 910;  
 Best Local Similarity 99.7%; Pred. No. 2.8e-179;  
 Matches 357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST 60  
 DB 1 MVLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGLTLLIWTYTRQDRDLLEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120  
 DB 61 AHSAGLTLLIWTYTRQDRDLLEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120

QY 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180  
 DB 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180

QY 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240  
 DB 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300  
 DB 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAVKQKVPAPRYTVE 359  
 DB 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAVKQKVPAPRYTVE 359

RESULT 14  
 US-10-282-162-28  
 ; Sequence 28, Application US/10282162  
 ; Patent No. 6927044  
 ; GENERAL INFORMATION:  
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
 ; FILE REFERENCE: REG 203-B-US  
 ; CURRENT APPLICATION NUMBER: US/10/282,162  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: 09/787,835

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; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-28

Query Match      52.6%; Score 1930; DB 2; Length 910;
Best Local Similarity 99.7%; Pred. No. 2.8e-179;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTLWCVVSLYFYGILQSDASERCDGGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYS 60
Db 1 MVLWCVVSLYFYGILQSDASERCDGGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYS 60

Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLPFRPTLLNDTGNCTCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLPFRPTLLNDTGNCTCMLRNTT 120

Qy 121 YCSKVAAPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGYPSSVKPTITWYMG 180
Db 121 YCSKVAAPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGYPSSVKPTITWYMG 180

Qy 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTKVVGSPKNA 240

Qy 241 VPPVIHSPNDHVYVEKPGGELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYVEKPGGELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300

Qy 301 SISHSRTEDETRTOILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTV 358
Db 301 SISHSRTEDETRTOILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTV 358

RESULT 15
US-10-282-162-34
; Sequence 34, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-34

Query Match      50.0%; Score 1833; DB 2; Length 900;
Best Local Similarity 100.0%; Pred. No. 8.6e-170;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 SERCDDGGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYSHTAHSAGLTLIYWTRQDRDL 80
Db 333 SERCDDGGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYSHTAHSAGLTLIYWTRQDRDL 392

Qy 81 EPINFRLPENRISKEKDVLPFRPTLLNDTGNCTCMLRNTTYCSKVAAPLEVVQKSCFNS 140
Db 81 EPINFRLPENRISKEKDVLPFRPTLLNDTGNCTCMLRNTTYCSKVAAPLEVVQKSCFNS 140
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Db 393 EPINFRLPENRISKEKDVLPFRPTLLNDTGNCTCMLRNTTYCSKVAAPLEVVQKSCFNS 452
Qy 141 PMKLPVHKLYIEYGIQRIITCPNVGYPSSVKPTITWYMGYKIQNFNNVIPEGNNLSFL 200
Db 453 PMKLPVHKLYIEYGIQRIITCPNVGYPSSVKPTITWYMGYKIQNFNNVIPEGNNLSFL 512
Qy 201 IALISNNGNYTCVVYTPENGRTFHLTRTLTKVVGSPKNAVPPVIHSPNDHVYVEKPG 260
Db 513 IALISNNGNYTCVVYTPENGRTFHLTRTLTKVVGSPKNAVPPVIHSPNDHVYVEKPG 572
Qy 261 ELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINESISHSRTEDETRTOILSIKK 320
Db 573 ELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINESISHSRTEDETRTOILSIKK 632
Qy 321 VTSEDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTV 359
Db 633 VTSEDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTV 671
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Job time : 28 secs